GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 11:44:23 ; Search time 636 Seconds
(without alignments)
10381.095 Million cell updates/sec

Title: US-10-066-521-5
Perfect score: 4035
Sequence: 1 atggaaggagacaaatcgct.....tcgaggggctggtgtcttaa 4035

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

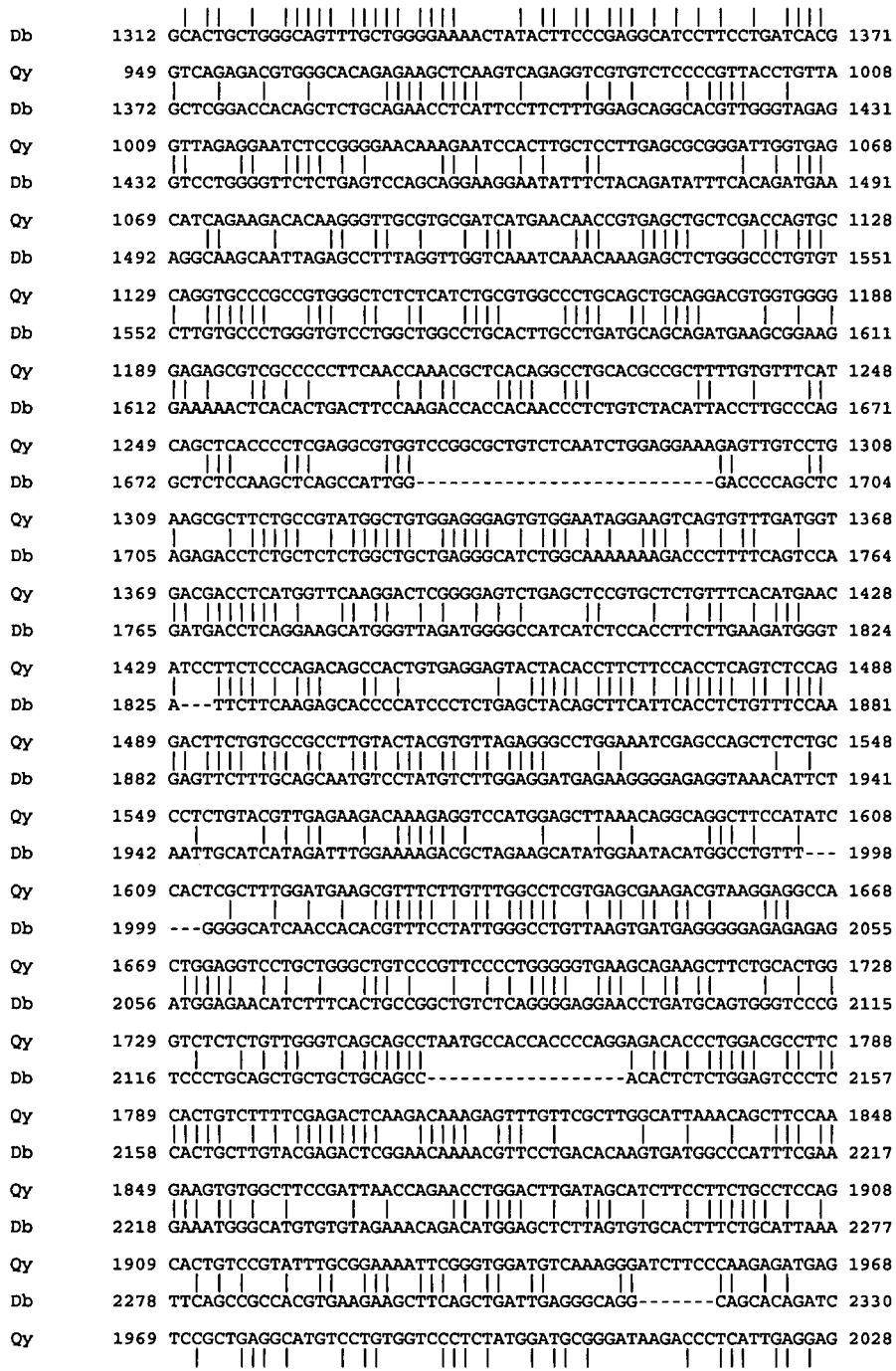
	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	221.4	5.5	4422	4	US-09-388-221B-1	Sequence 1, Appli
	2	221.4	5.5	4556	4	US-09-388-221B-9	Sequence 9, Appli
	3	220.6	5.5	4200	4	US-09-388-221B-3	Sequence 3, Appli
	4	220.6	5.5	4332	4	US-09-388-221B-5	Sequence 5, Appli
	5	220.6	5.5	4466	4	US-09-388-221B-11	Sequence 11, Appl
	6	183.8	4.6	1371	2	US-08-910-731-1	Sequence 1, Appli
	7	183.8	4.6	1371	2	US-08-795-395-1	Sequence 1, Appli
	8	182.4	4.5	1386	2	US-08-910-731-5	Sequence 5, Appli
	9	180.8	4.5	1371	2	US-08-910-731-7	Sequence 7, Appli
	10	175.8	4.4	1374	2	US-08-910-731-3	Sequence 3, Appli
	11	175.8	4.4	1374	2	US-08-795-395-3	Sequence 3, Appli
c	12	61	1.5	7218	1	US-08-232-463-14	Sequence 14, Appl
	13	60	1.5	376	4	US-09-023-655-395	Sequence 395, App
	14	51.4	1.3	298336	4	US-09-949-016-16600	Sequence 16600, A
c	15	50.8	1.3	64309	4	US-09-949-016-14581	Sequence 14581, A
	16	47.4	1.2	4485	4	US-09-949-016-3209	Sequence 3209, Ap
	17	47.4	1.2	4485	4	US-10-014-269-1	Sequence 1, Appli
	18	47.4	1.2	4486	4	US-10-014-269-33	Sequence 33, Appl
	19	46.6	1.2	1276	3	US-09-177-325-2	Sequence 2, Appli
	20	46.6	1.2	1276	3	US-09-411-812A-2	Sequence 2, Appli
	21	46.6	1.2	1276	3	US-09-590-113-2	Sequence 2, Appli
	22	46.4	1.1	2780	4	US-09-620-312D-358	Sequence 358, App
c	23	45	1.1	929	4	US-09-671-317-14	Sequence 14, Appl
	24	44.8	1.1	1620	4	US-09-134-000C-340	Sequence 340, App
c	25	43.4	1.1	1001	4	US-09-671-317-439	Sequence 439, App
	26	43.2	1.1	193303	4	US-09-497-855A-37	Sequence 37, Appl
	27	43.2	1.1	193303	4	US-09-497-855A-44	Sequence 44, Appl
	28	42.8	1.1	1449	4	US-09-248-796A-4693	Sequence 4693, Ap
	29	42.8	1.1	767677	4	US-09-949-016-12147	Sequence 12147, A
	30	42.8	1.1	767677	4	US-09-949-016-17361	Sequence 17361, A
	31	42.6	1.1	693	4	US-09-252-991A-11050	Sequence 11050, A
	32	42.6	1.1	1005	4	US-09-252-991A-10976	Sequence 10976, A
c	33	42.6	1.1	1185	4	US-09-252-991A-11203	Sequence 11203, A
c	34	42.4	1.1	150394	4	US-09-949-016-13042	Sequence 13042, A
	35	42.2	1.0	38566	4	US-09-949-016-15271	Sequence 15271, A
	36	42.2	1.0	38566	4	US-09-949-016-15272	Sequence 15272, A
	37	42	1.0	3117	4	US-09-614-221A-275	Sequence 275, App
	38	41.8	1.0	7044	4	US-09-949-016-14113	Sequence 14113, A
	39	41.6	1.0	2223	1	US-08-257-073-4	Sequence 4, Appli
c	40	41.4	1.0	505	4	US-09-621-976-15639	Sequence 15639, A
c	41	41.2	1.0	810	4	US-09-614-221A-103	Sequence 103, App
	42	41.2	1.0	43795	3	US-08-742-185-101	Sequence 101, App
	43	41	1.0	505	4	US-09-621-976-15639	Sequence 15639, A
c	44	41	1.0	10391	4	US-09-902-540-958	Sequence 958, App
	45	40.4	1.0	240157	4	US-09-949-016-16264	Sequence 16264, A

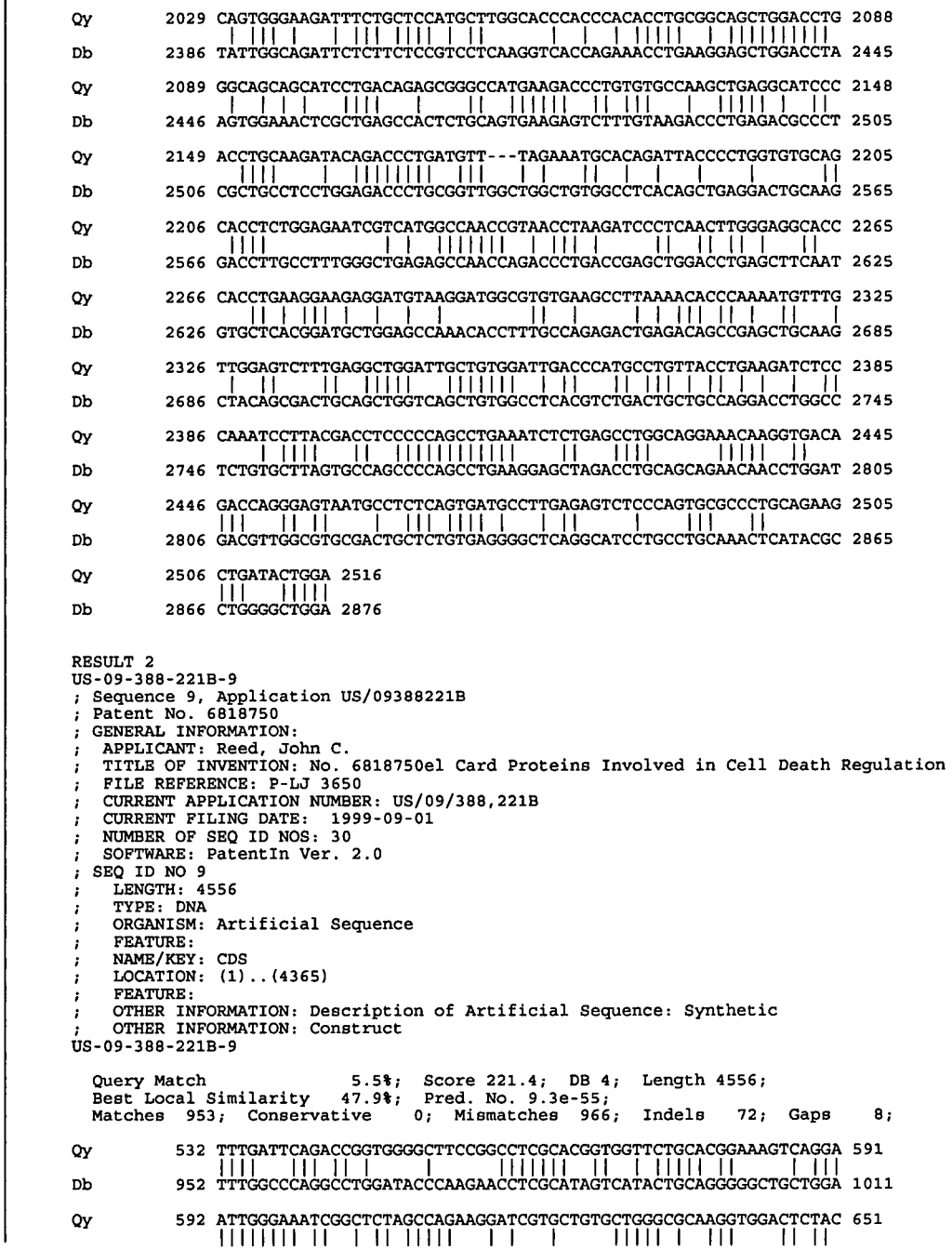
ALIGNMENTS

RESULT 1
US-09-388-221B-1
; Sequence 1, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4422
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4422)
US-09-388-221B-1

Query Match 5.5%; Score 221.4; DB 4; Length 4422;
Best Local Similarity 47.9%; Pred. No. 9.1e-55;
Matches 953; Conservative 0; Mismatches 966; Indels 72; Gaps 8;

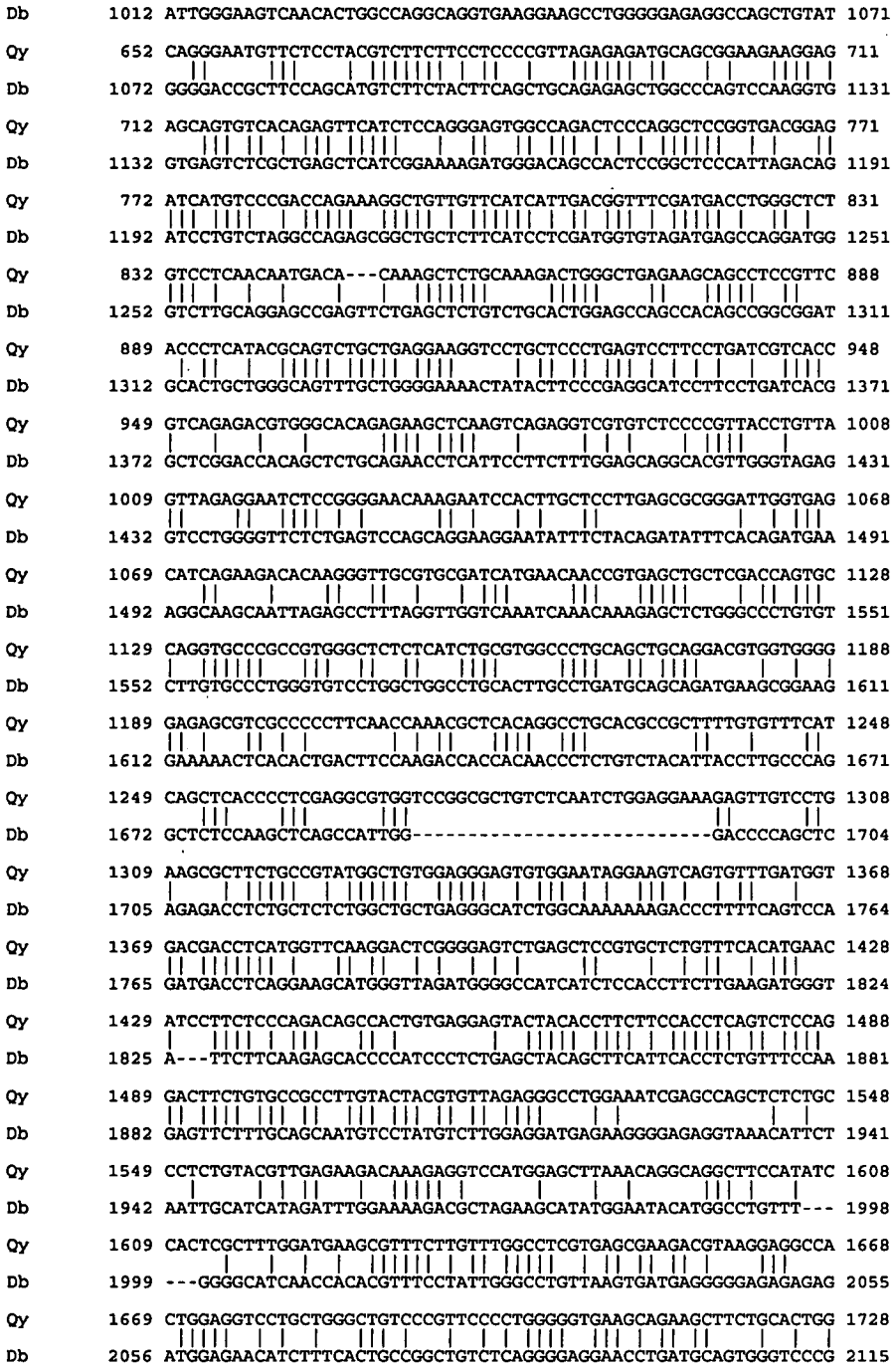
```
Qy       532 TTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGA 591
            |||| ||| || |  |  |||||||  ||  | ||||| ||  |  | |||
Db       952 TTTGGCCCAGGCCTGGATACCCAAGAACCTCGCATAGTCATACTGCAGGGGGCTGCTGGA 1011

Qy       592 ATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTAC 651
            |||||||| ||  | || |||||  | |  |  |||||  |  |||  || ||
Db      1012 ATTGGGAAGTCAACACTGGCCAGGCAGGTGAAGGAAGCCTGGGGGAGAGGCCAGCTGTAT 1071

Qy       652 CAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAG 711
              ||   |||   | |||||||| | ||  |  ||||| ||  | |  |||| |
Db      1072 GGGGACCGCTTCCAGCATGTCTTCTACTTCAGCTGCAGAGAGCTGGCCCAGTCCAAGGTG 1131

Qy       712 AGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAG 771
            ||| || | ||| |||||  |  ||  || ||| | | | ||||||  | |  ||
Db      1132 GTGAGTCTCGCTGAGCTCATCGGAAAAGATGGGACAGCCACTCCGGCTCCCATTAGACAG 1191

Qy       772 ATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCT 831
            ||| ||||  | |||||  ||||| | |||||| | || ||| | |||||  || |
Db      1192 ATCCTGTCTAGGCCAGAGCGGCTGCTCTTCATCCTCGATGGTGTAGATGAGCCAGGATGG 1251

Qy       832 GTCCTCAACAATGACA---CAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTC 888
            ||| |  |  |   |  | |||||||    |||||   ||  |||||  ||
Db      1252 GTCTTGCAGGAGCCGAGTTCTGAGCTCTGTCTGCACTGGAGCCAGCCACAGCCGGCGGAT 1311

Qy       889 ACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACC 948
```

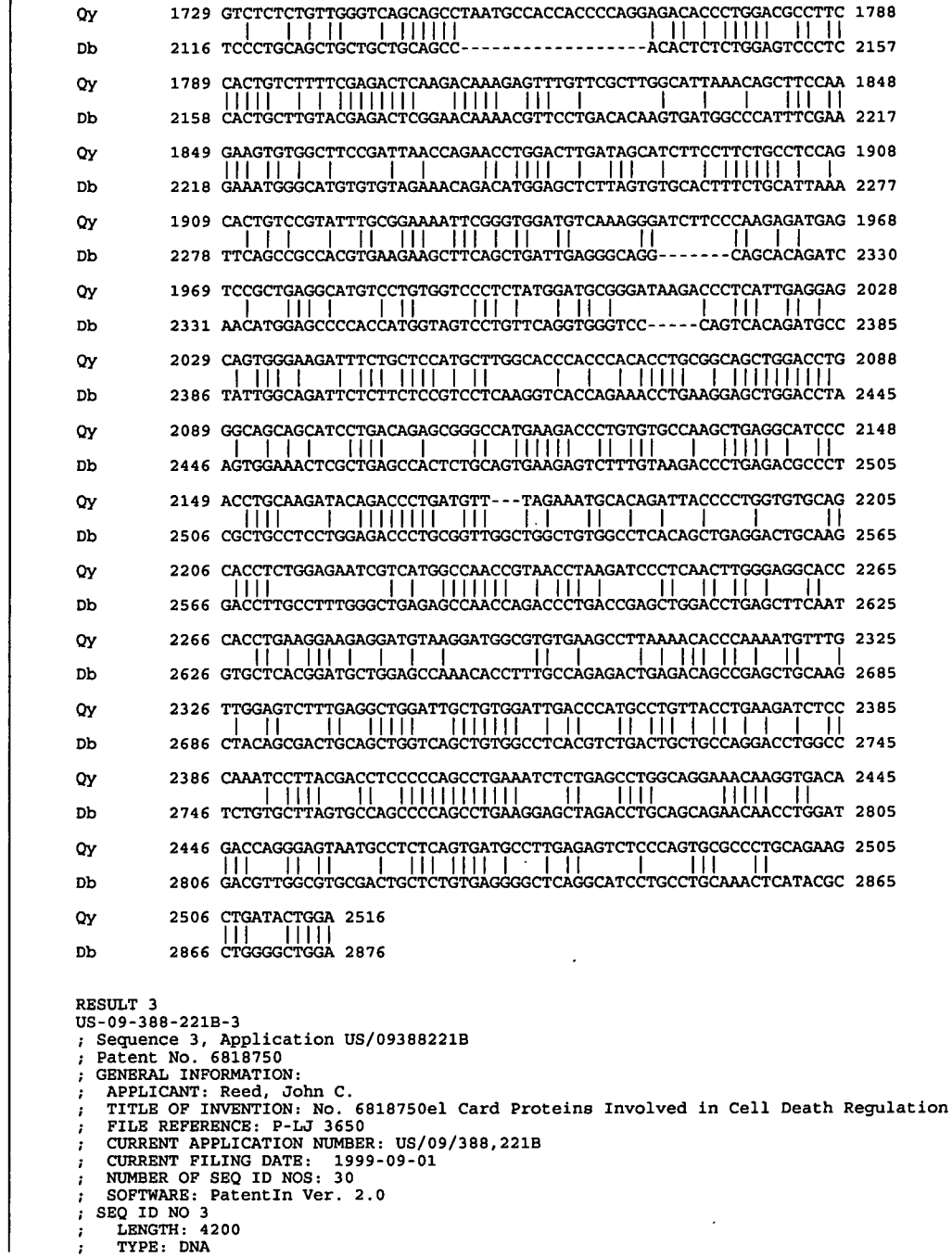




RESULT 2
US-09-388-221B-9
; Sequence 9, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 4556
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4365)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
US-09-388-221B-9

Query Match 5.5%; Score 221.4; DB 4; Length 4556;
Best Local Similarity 47.9%; Pred. No. 9.3e-55;
Matches 953; Conservative 0; Mismatches 966; Indels 72; Gaps 8;



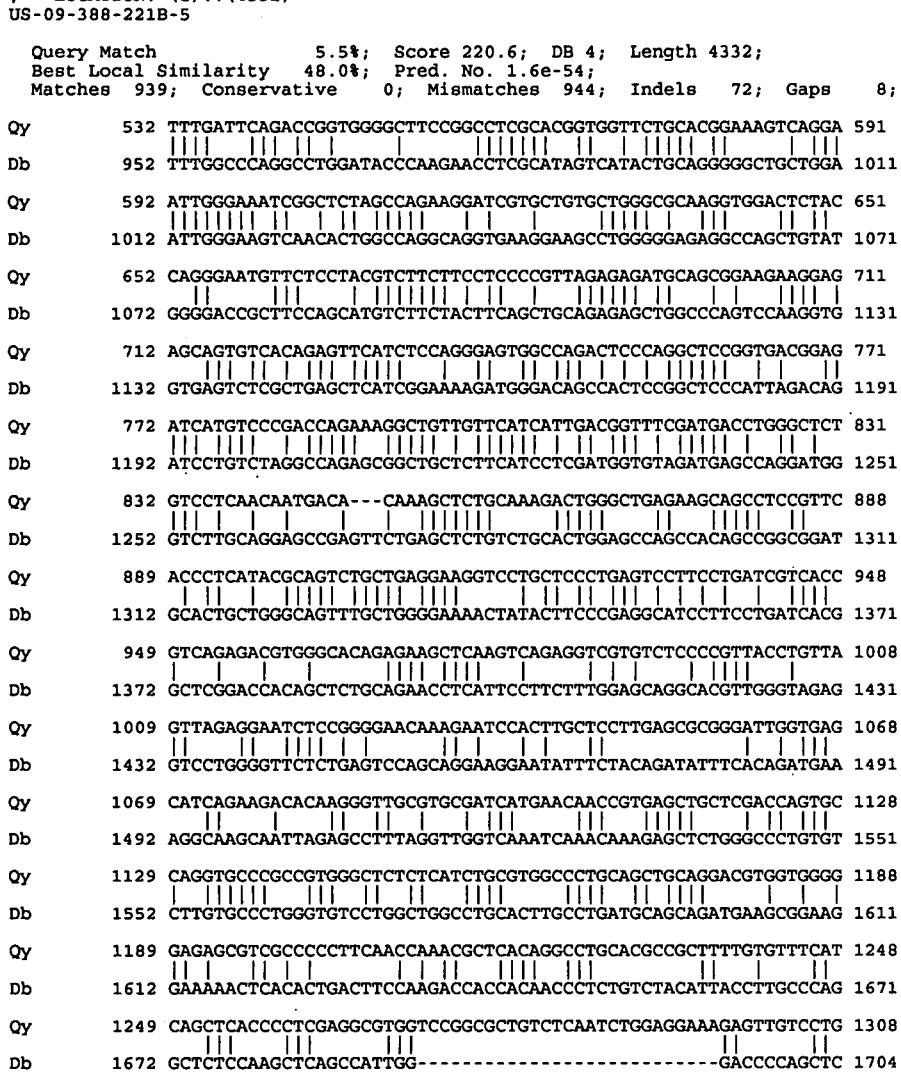


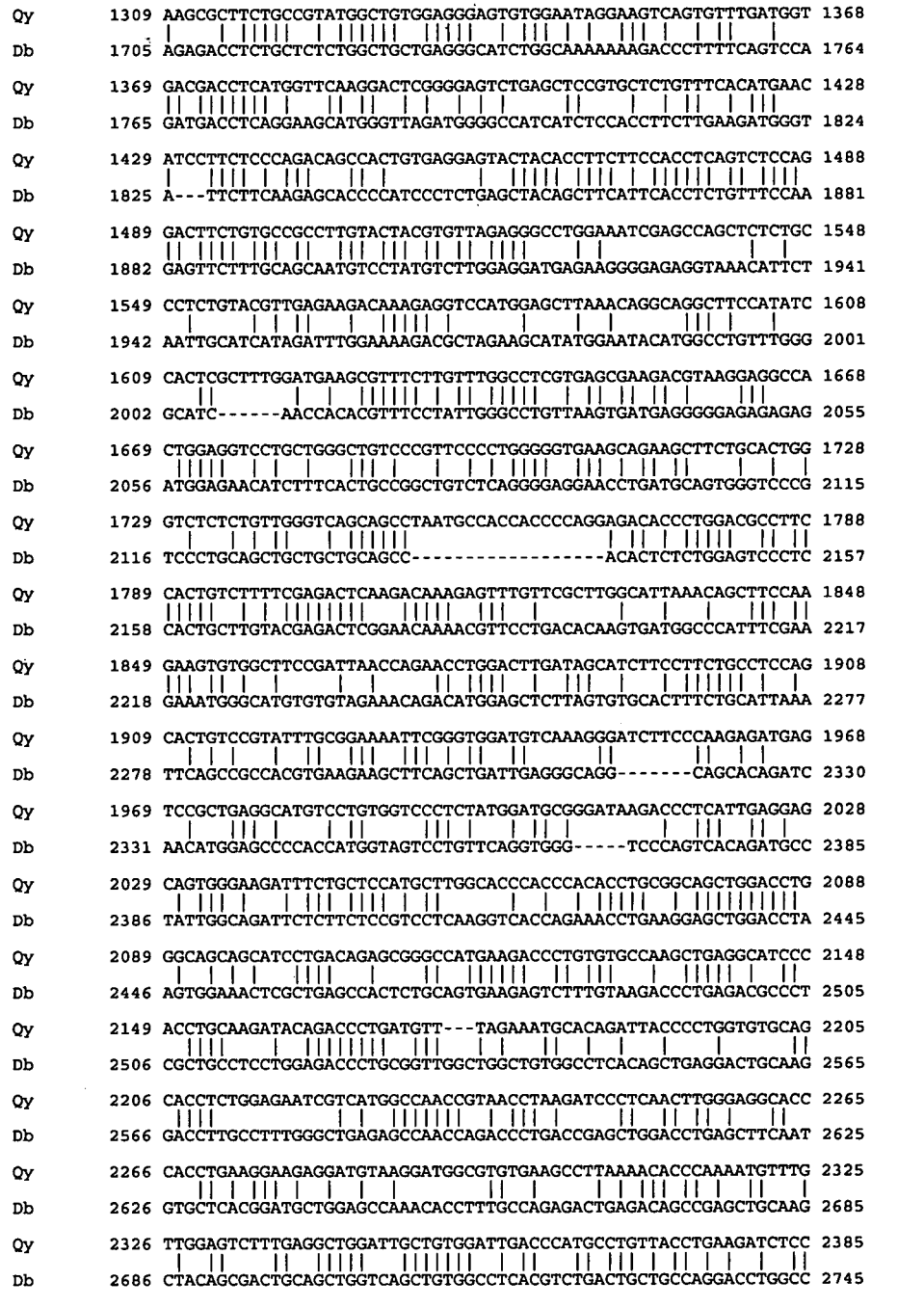
```
RESULT 3
US-09-388-221B-3
; Sequence 3, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
;  APPLICANT: Reed, John C.
;  TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
;  FILE REFERENCE: P-LJ 3650
;  CURRENT APPLICATION NUMBER: US/09/388,221B
;  CURRENT FILING DATE:  1999-09-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 4200
;   TYPE: DNA
```

```
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(4197)
US-09-388-221B-3

  Query Match             5.5%;  Score 220.6;  DB 4;  Length 4200;
  Best Local Similarity   48.0%;  Pred. No. 1.5e-54;
  Matches  939;  Conservative    0;  Mismatches  944;  Indels   72;  Gaps    8;

Qy        532 TTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGA 591
              ||||   ||| || |     |      |||||||  ||  | |||||  ||      | |||
Db        952 TTTGGCCCAGGCCTGGATACCCAAGAACCTCGCATAGTCATACTGCAGGGGGCTGCTGGA 1011

Qy        592 ATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTAC 651
              ||||||||  ||   | ||  |||||    | |    |      |||||  |  |||     || ||
Db       1012 ATTGGGAAGTCAACACTGGCCAGGCAGGTGAAGGAAGCCTGGGGGAGAGGCCAGCTGTAT 1071

Qy        652 CAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAG 711
                ||      |||     | |||||||  | ||  |   ||||||  ||    | |    |||| |
Db       1072 GGGGACCGCTTCCAGCATGTCTTCTACTTCAGCTGCAGAGAGCTGGCCCAGTCCAAGGTG 1131

Qy        712 AGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAG 771
              |||  ||  | |||  |||||    |  ||   ||  |||  |  |  ||||||   |  |    ||
Db       1132 GTGAGTCTCGCTGAGCTCATCGGAAAAGATGGGACAGCCACTCCGGCTCCCATTAGACAG 1191

Qy        772 ATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCT 831
              |||  ||||   | |||||  |||||  | |||||||  | ||  |||  | |||||  |   ||  |
Db       1192 ATCCTGTCTAGGCCAGAGCGGCTGCTCTTCATCCTCGATGGTGTAGATGAGCCAGGATGG 1251

Qy        832 GTCCTCAACAATGACA---CAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTC 888
              |||  |   |  |     |   |  |||||||      |||||    ||   |||||  ||
Db       1252 GTCTTGCAGGAGCCGAGTTCTGAGCTCTGTCTGCACTGGAGCCAGCCACAGCCGGCGGAT 1311

Qy        889 ACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACC 948
              | ||  |  |||||  |||||  ||||     | ||  ||  |||  |  |  |   |  ||||
Db       1312 GCACTGCTGGGCAGTTTGCTGGGGAAAACTATACTTCCCGAGGCATCCTTCCTGATCACG 1371

Qy        949 GTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTA 1008
              |    |    |    |       ||||  ||||    |       | | |     | ||||    |
Db       1372 GCTCGGACCACAGCTCTGCAGAACCTCATTCCTTCTTTGGAGCAGGCACGTTGGGTAGAG 1431

Qy       1009 GTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAG 1068
              ||    ||  ||||  | |      ||  |    |  |   ||                |  | |||
Db       1432 GTCCTGGGGTTCTCTGAGTCCAGCAGGAAGGAATATTTCTACAGATATTTCACAGATGAA 1491

Qy       1069 CATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGC 1128
              ||    |   ||  ||  |   | |||     |||   ||||||    | || |||
Db       1492 AGGCAAGCAATTAGAGCCTTTAGGTTGGTCAAATCAAACAAAGAGCTCTGGGCCCTGTGT 1551

Qy       1129 CAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGG 1188
              |  ||||||   |||  ||  ||   ||||     ||||  ||  ||||      |  |  |
Db       1552 CTTGTGCCCTGGGTGTCCTGGCTGGCCTGCACTTGCCTGATGCAGCAGATGAAGCGGAAG 1611

Qy       1189 GAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCAT 1248
              || |   ||  | |       | | ||   ||||  |||          ||   |    ||
Db       1612 GAAAAACTCACACTGACTTCCAAGACCACCACAACCCTCTGTCTACATTACCTTGCCCAG 1671

Qy       1249 CAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTG 1308
                |||     |||       |||                              ||      ||
Db       1672 GCTCTCCAAGCTCAGCCATTGG--------------------------GACCCCAGCTC 1704

Qy       1309 AAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGT 1368
              |     | |||||  | ||||||  |||||   | |||  | |   |||  |  |  ||    |
Db       1705 AGAGACCTCTGCTCTCTGGCTGCTGAGGGCATCTGGCAAAAAAAGACCCTTTTCAGTCCA 1764

Qy       1369 GACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAAC 1428
              ||  |||||||  |   || ||  |  |  | |  |      ||     |  ||  | |||
Db       1765 GATGACCTCAGGAAGCATGGGTTAGATGGGGCCATCATCTCCACCTTCTTGAAGATGGGT 1824

Qy       1429 ATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAG 1488
              |   |||| | |||    || |          |  |||||  |||| | ||||||  || ||||
Db       1825 A---TTCTTCAAGAGCACCCCATCCCTCTGAGCTACAGCTTCATTCACCTCTGTTTCCAA 1881

Qy       1489 GACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGC 1548
              || |||| ||| ||  ||| ||| || || ||||     | |              |  |
Db       1882 GAGTTCTTTGCAGCAATGTCCTATGTCTTGGAGGATGAGAAGGGGAGAGGTAAACATTCT 1941

Qy       1549 CCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATC 1608
                |     | | ||   | |||||  |       |     |   |       ||| |   |
Db       1942 AATTGCATCATAGATTTGGAAAAGACGCTAGAAGCATATGGAATACATGGCCTGTTTGGG 2001

Qy       1609 CACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCA 1668
                ||        |  |  |||||| | || |||||  | ||  || ||  |     |||
Db       2002 GCATC------AACCACACGTTTCCTATTGGGCCTGTTAAGTGATGAGGGGGAGAGAGAG 2055

Qy       1669 CTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGG 1728
                |||||  | |  |   ||| |   |  | | ||||  ||| | || ||    |  |  |
Db       2056 ATGGAGAACATCTTTCACTGCCGGCTGTCTCAGGGGAGGAACCTGATGCAGTGGGTCCCG 2115

Qy       1729 GTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTC 1788
                |   | | ||   | ||||||                    | || | |||||  || ||
Db       2116 TCCCTGCAGCTGCTGCTGCAGCC-----------------ACACTCTCTGGAGTCCCTC 2157

Qy       1789 CACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAA 1848
              |||||  | | ||||||||   |||||  |||  |      |   |   |  ||| ||
Db       2158 CACTGCTTGTACGAGACTCGGAACAAAACGTTCCTGACACAAGTGATGGCCCATTTCGAA 2217

Qy       1849 GAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAG 1908
              ||| || |  |     |  |    || ||||  |  |||  |  | ||||||  | |
Db       2218 GAAATGGGCATGTGTGTAGAAACAGACATGGAGCTCTTAGTGTGCACTTTCTGCATTAAA 2277

Qy       1909 CACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAG 1968
                | | |   |  ||  |||  ||| | ||  ||      ||    ||  ||  ||
Db       2278 TTCAGCCGCCACGTGAAGAAGCTTCAGCTGATTGAGGGCAGG-------CAGCACAGATC 2330

Qy       1969 TCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAG 2028
                |   ||| |    | ||     ||| |   | || |        |  |||  || |
Db       2331 AACATGGAGCCCCACCATGGTAGTCCTGTTCAGGTGGG-----TCCCAGTCACAGATGCC 2385

Qy       2029 CAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTG 2088
                | ||| |   | ||| |||| | ||       |  |  | |||||  | ||||||||||
Db       2386 TATTGGCAGATTCTCTTCTCCGTCCTCAAGGTCACCAGAAACCTGAAGGAGCTGGACCTA 2445

Qy       2089 GGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCC 2148
                |  | | |    |||  |    || ||||||  || |||   |  |||||  |  ||
Db       2446 AGTGGAAACTCGCTGAGCCACTCTGCAGTGAAGAGTCTTTGTAAGACCCTGAGACGCCCT 2505

Qy       2149 ACCTGCAAGATACAGACCCTGATGTT---TAGAAATGCACAGATTACCCCTGGTGTGCAG 2205
                ||||    |  |||||||| |||   | |  ||  |  |  |    |      ||
Db       2506 CGCTGCCTCCTGGAGACCCTGCGGTTGGCTGGCTGTGGCCTCACAGCTGAGGACTGCAAG 2565

Qy       2206 CACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACC 2265
                ||||          | |  |||||||  | |||  |     ||  || || |   ||
Db       2566 GACCTTGCCTTTGGGCTGAGAGCCAACCAGACCCTGACCGAGCTGGACCTGAGCTTCAAT 2625

Qy       2266 CACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTG 2325
                || | |||  |    |       || |     | | |||  || |  ||   |
Db       2626 GTGCTCACGGATGCTGGAGCCAAACACCTTTGCCAGAGACTGAGACAGCCGAGCTGCAAG 2685

Qy       2326 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2385
                |  ||     ||  |||||   |||||||  | ||   || ||| | || | |   | ||
Db       2686 CTACAGCGACTGCAGCTGGTCAGCTGTGGCCTCACGTCTGACTGCTGCCAGGACCTGGCC 2745

Qy       2386 CAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACA 2445
                | ||||    ||  ||||||||||||     ||   ||||        |||||  ||
Db       2746 TCTGTGCTTAGTGCCAGCCCCAGCCTGAAGGAGCTAGACCTGCAGCAGAACAACCTGGAT 2805

Qy       2446 GACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAG 2480
                |||   || ||      | |||  |||| |   | ||
Db       2806 GACGTTGGCGTGCGACTGCTCTGTGAGGGGCTCAG 2840


RESULT 4
US-09-388-221B-5
; Sequence 5, Application US/09388221B
```

; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4332
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4332)
US-09-388-221B-5

Query Match 5.5%; Score 220.6; DB 4; Length 4332;
Best Local Similarity 48.0%; Pred. No. 1.6e-54;
Matches 939; Conservative 0; Mismatches 944; Indels 72; Gaps 8;





```
Qy       2386 CAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACA 2445
             | ||||   ||  ||||||||||||   ||   ||||    |||||  ||
Db       2746 TCTGTGCTTAGTGCCAGCCCCAGCCTGAAGGAGCTAGACCTGCAGCAGAACAACCTGGAT 2805

Qy       2446 GACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAG 2480
              |||   || ||    |  ||| |||| |   | ||
Db       2806 GACGTTGGCGTGCGACTGCTCTGTGAGGGGCTCAG 2840


RESULT 5
US-09-388-221B-11
; Sequence 11, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
;  APPLICANT: Reed, John C.
;  TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
;  FILE REFERENCE: P-LJ 3650
;  CURRENT APPLICATION NUMBER: US/09/388,221B
;  CURRENT FILING DATE:  1999-09-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 4466
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(4272)
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Construct
US-09-388-221B-11

  Query Match             5.5%;  Score 220.6;  DB 4;  Length 4466;
  Best Local Similarity   48.0%;  Pred. No. 1.6e-54;
  Matches  939;  Conservative    0;  Mismatches  944;  Indels   72;  Gaps    8;

Qy        532 TTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGA 591
              ||||   ||| || |     |      |||||||  ||  | |||||  ||      | |||
Db        952 TTTGGCCCAGGCCTGGATACCCAAGAACCTCGCATAGTCATACTGCAGGGGGCTGCTGGA 1011

Qy        592 ATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTAC 651
              |||||||| ||  | || |||||    | |    |     |||||  |  |||    || ||
Db       1012 ATTGGGAAGTCAACACTGGCCAGGCAGGTGAAGGAAGCCTGGGGGAGAGGCCAGCTGTAT 1071

Qy        652 CAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAG 711
               ||     |||    | |||||||  | ||   |   ||||||  ||    | |    |||| |
Db       1072 GGGGACCGCTTCCAGCATGTCTTCTACTTCAGCTGCAGAGAGCTGGCCCAGTCCAAGGTG 1131

Qy        712 AGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAG 771
                |||  ||  |  |||  |||||    |   ||   ||  |||  |  |  ||||||   |  |    ||
Db       1132 GTGAGTCTCGCTGAGCTCATCGGAAAAGATGGGACAGCCACTCCGGCTCCCATTAGACAG 1191

Qy        772 ATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCT 831
              |||  ||||   |  |||||   |||||  |  ||||||  |  ||  |||  |  |||||  |   ||  |
Db       1192 ATCCTGTCTAGGCCAGAGCGGCTGCTCTTCATCCTCGATGGTGTAGATGAGCCAGGATGG 1251

Qy        832 GTCCTCAACAATGACA---CAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTC 888
              |||  |   |   |    |  |||||||      |||||    ||   |||||  ||
Db       1252 GTCTTGCAGGAGCCGAGTTCTGAGCTCTGTCTGCACTGGAGCCAGCCACAGCCGGCGGAT 1311

Qy        889 ACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACC 948
              | ||  |  ||||| |||||  |||| |      | ||  ||  |||  |  |  |   |  ||||
Db       1312 GCACTGCTGGGCAGTTTGCTGGGGAAAACTATACTTCCCGAGGCATCCTTCCTGATCACG 1371

Qy        949 GTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTA 1008
              |    |   |      |||| ||||    |     |  |  |    | ||||    |
Db       1372 GCTCGGACCACAGCTCTGCAGAACCTCATTCCTTCTTTGGAGCAGGCACGTTGGGTAGAG 1431

Qy       1009 GTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAG 1068
              ||    ||  |||| | |      || |   | |   ||                |  | |||
Db       1432 GTCCTGGGGTTCTCTGAGTCCAGCAGGAAGGAATATTTCTACAGATATTTCACAGATGAA 1491
```

```
Qy       1069 CATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGC 1128
              ||    |    ||  ||  |  | |||     |||   |||||     | || |||
Db       1492 AGGCAAGCAATTAGAGCCTTTAGGTTGGTCAAATCAAACAAAGAGCTCTGGGCCCTGTGT 1551

Qy       1129 CAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGG 1188
              |  ||||||   |||  ||  ||   ||||      ||||  || ||||      |  |  |
Db       1552 CTTGTGCCCTGGGTGTCCTGGCTGGCCTGCACTTGCCTGATGCAGCAGATGAAGCGGAAG 1611

Qy       1189 GAGAGCGTCGCCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCAT 1248
              || |   || | |          | | ||   ||||  |||           ||    |    ||
Db       1612 GAAAAACTCACACTGACTTCCAAGACCACCACAACCCTCTGTCTACATTACCTTGCCCAG 1671

Qy       1249 CAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTG 1308
                 |||     |||      |||                                ||      ||
Db       1672 GCTCTCCAAGCTCAGCCATTGG--------------------------GACCCCAGCTC 1704

Qy       1309 AAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGT 1368
              |    | |||||  | ||||||  |||||  | |||  | |  |||  |  | ||   |
Db       1705 AGAGACCTCTGCTCTCTGGCTGCTGAGGGCATCTGGCAAAAAAAGACCCTTTTCAGTCCA 1764

Qy       1369 GACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAAC 1428
              || |||||||  |   || ||  |  |  |  |      ||     |  | ||  | |||
Db       1765 GATGACCTCAGGAAGCATGGGTTAGATGGGGCCATCATCTCCACCTTCTTGAAGATGGGT 1824

Qy       1429 ATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAG 1488
              |   |||| | |||    || |      |  ||||| |||| | ||||||  || ||||
Db       1825 A---TTCTTCAAGAGCACCCCATCCCTCTGAGCTACAGCTTCATTCACCTCTGTTTCCAA 1881

Qy       1489 GACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGC 1548
              || |||| ||| ||  ||| ||| || || ||||    | ||              |  |
Db       1882 GAGTTCTTTGCAGCAATGTCCTATGTCTTGGAGGATGAGAAGGGGAGAGGTAAACATTCT 1941

Qy       1549 CCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATC 1608
                |     | | ||   | |||||  |       |     |  |       |||  |   |
Db       1942 AATTGCATCATAGATTTGGAAAAGACGCTAGAAGCATATGGAATACATGGCCTGTTTGGG 2001

Qy       1609 CACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCA 1668
                ||     |  |  |||||| | || |||||  | || || || |    |||
Db       2002 GCATC------AACCACACGTTTCCTATTGGGCCTGTTAAGTGATGAGGGGGAGAGAGAG 2055

Qy       1669 CTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGG 1728
                |||||  |  |   ||| |   |  | | ||||  ||| | || ||    |  |  |
Db       2056 ATGGAGAACATCTTTCACTGCCGGCTGTCTCAGGGGAGGAACCTGATGCAGTGGGTCCCG 2115

Qy       1729 GTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTC 1788
                |  | | ||   | ||||||                    | || | |||||  || ||
Db       2116 TCCCTGCAGCTGCTGCTGCAGCC-----------------ACACTCTCTGGAGTCCCTC 2157

Qy       1789 CACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAA 1848
              |||||  | | ||||||||   |||||  |||  |    |   |  |  |||  ||
Db       2158 CACTGCTTGTACGAGACTCGGAACAAAACGTTCCTGACACAAGTGATGGCCCATTTCGAA 2217

Qy       1849 GAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAG 1908
              ||| || |  |      |  |     || ||||  |  |||  |  | ||||||  |  |
Db       2218 GAAATGGGCATGTGTGTAGAAACAGACATGGAGCTCTTAGTGTGCACTTTCTGCATTAAA 2277

Qy       1909 CACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAG 1968
                | |  |   |  ||  |||  ||| | ||  ||      ||    ||  | |
Db       2278 TTCAGCCGCCACGTGAAGAAGCTTCAGCTGATTGAGGGCAGG-------CAGCACAGATC 2330

Qy       1969 TCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAG 2028
                |   ||| |   | ||    ||| |   | || |          |  |||  || |
Db       2331 AACATGGAGCCCCACCATGGTAGTCCTGTTCAGGTGGG-----TCCCAGTCACAGATGCC 2385

Qy       2029 CAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTG 2088
              | ||| |   | ||| |||| | ||       |  |  | |||||  | ||||||||||
Db       2386 TATTGGCAGATTCTCTTCTCCGTCCTCAAGGTCACCAGAAACCTGAAGGAGCTGGACCTA 2445

Qy       2089 GGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCC 2148
              |  | | |   ||||    |  ||  |||||| || |||    |  |||||  |  ||
Db       2446 AGTGGAAACTCGCTGAGCCACTCTGCAGTGAAGAGTCTTTGTAAGACCCTGAGACGCCCT 2505

Qy       2149 ACCTGCAAGATACAGACCCTGATGTT---TAGAAATGCACAGATTACCCCTGGTGTGCAG 2205
```

```
Db       2506 CGCTGCCTCCTGGAGACCCTGCGGTTGGCTGGCTGTGGCCTCACAGCTGAGGACTGCAAG 2565

Qy       2206 CACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACC 2265

Db       2566 GACCTTGCCTTTGGGCTGAGAGCCAACCAGACCCTGACCGAGCTGGACCTGAGCTTCAAT 2625

Qy       2266 CACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTG 2325

Db       2626 GTGCTCACGGATGCTGGAGCCAAACACCTTTGCCAGAGACTGAGACAGCCGAGCTGCAAG 2685

Qy       2326 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2385

Db       2686 CTACAGCGACTGCAGCTGGTCAGCTGTGGCCTCACGTCTGACTGCTGCCAGGACCTGGCC 2745

Qy       2386 CAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACA 2445

Db       2746 TCTGTGCTTAGTGCCAGCCCCAGCCTGAAGGAGCTAGACCTGCAGCAGAACAACCTGGAT 2805

Qy       2446 GACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAG 2480

Db       2806 GACGTTGGCGTGCGACTGCTCTGTGAGGGGCTCAG 2840


RESULT 6
US-08-910-731-1
; Sequence 1, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1371 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1368
US-08-910-731-1

  Query Match             4.6%;  Score 183.8;  DB 2;  Length 1371;
  Best Local Similarity   47.2%;  Pred. No. 7e-44;
  Matches  591;  Conservative    0;  Mismatches  657;  Indels    3;  Gaps    1;

Qy       2016 CCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCG 2075

Db        102 CCTCACGGAGGAGCACTGCAAGGACATCGGTTCTGCCCTCCGGGCCAACCCCTCCCTGAC 161

Qy       2076 GCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAA 2135

Db        162 CGAGCTCTGCCTCCGCACCAACGAGCTGGGCGATGCCGGCGTGCACCTGGTGCTGCAGGG 221

Qy       2136 GCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCC- 2194

Db        222 CCTGCAGAGCCCCACCTGCAAGATCCAGAAGCTCAGCCTGCAGAACTGCTCCCTGACCGA 281

Qy       2195 --CTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAA 2252

Db        282 GGCGGGCTGCGGGGTCCTGCCCAGCACGCTGCGCTCCCTGCCCACGCTGCGGGAGCTGCA 341

Qy       2253 CTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACA 2312

Db        342 TCTCAGCGACAACCCACTGGGGGACGCCGGCCTGCGGCTGCTCTGTGAGGGGCTCCTGGA 401

Qy       2313 CCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTA 2372

Db        402 CCCCCAGTGCCACCTGGAGAAGCTGCAGTTGGAGTACTGCCGCCTGACGGCCGCCAGCTG 461

Qy       2373 CCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGG 2432

Db        462 CGAGCCCCTGGCCTCGGTGCTCAGGGCCACGCGGGCCTTGAAGGAGCTCACGGTGAGCAA 521

Qy       2433 AAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTG 2492

Db        522 CAACGACATCGGCGAGGCCGGCGCCCGGGTGCTGGGCCAGGGTCTGGCAGACTCTGCCTG 581

Qy       2493 CGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCT 2552

Db        582 CCAGCTGGAGACGCTCAGGCTGGAGAACTGCGGTCTCACGCCAGCCAACTGCAAAGACCT 641

Qy       2553 GGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCT 2612

Db        642 GTGCGGAATTGTGGCCTCCCAGGCCTCGCTGAGGGAGCTTGACCTGGGCAGCAACGGGCT 701

Qy       2613 GGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCA 2672

Db        702 GGGCGACGCGGGCATAGCCGAGCTGTGCCCCGGGCTCTTGAGCCCCGCCTCCCGCCTCAA 761

Qy       2673 GAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGC 2732

Db        762 GACCCTGTGGCTCTGGGAGTGTGACATCACCGCCAGTGGCTGCAGAGACCTCTGCCGTGT 821

Qy       2733 GCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAA 2792

Db        822 CCTCCAGGCCAAGGAGACCCTGAAGGAGCTCAGTCTGGCGGGCAACAAGCTGGGCGACGA 881

Qy       2793 TGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGA 2852

Db        882 GGGCGCCCGGCTGCTGTGCGAGAGCCTGCTGCAGCCCGGCTGCCAGCTGGAGTCCCTGTG 941

Qy       2853 GTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAG 2912

Db        942 GGTGAAGTCCTGCAGCCTCACGGCGGCCTGCTGCCAGCACGTCAGCTTGATGCTGACCCA 1001

Qy       2913 GAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGC 2972

Db       1002 GAACAAGCATCTCCTGGAACTTCAGTTGAGCAGCAACAAGCTGGGTGACTCTGGCATCCA 1061

Qy       2973 TGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGC 3032
```

```
Db       1062 GGAGCTGTGCCAGGCCCTGAGCCAGCCGGGCACCACACTGCGGGTGCTCTGTCTTGGGGA 1121

Qy       3033 ATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCA 3092

Db       1122 CTGTGAGGTGACCAACAGCGGCTGCAGCAGCCTCGCCTCGCTCCTGCTGGCCAACCGCAG 1181

Qy       3093 TCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTG 3152

Db       1182 CCTGCGAGAGCTGGACCTGAGCAACAACTGTGTGGGCGACCCGGGCGTCCTGCAGCTGCT 1241

Qy       3153 TTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTA 3212

Db       1242 GGGGAGCCTGGAGCAGCCGGGCTGCGCCCTGGAGCAGCTGGTCCTGTACGACACCTACTG 1301

Qy       3213 CCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCG 3263

Db       1302 GACGGAGGAGGTGGAGGACCGCCTGCAGGCCCTGGAGGGGAGCAAGCCCGG 1352


RESULT 7
US-08-795-395-1
; Sequence 1, Application US/08795395
; Patent No. 5965399
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Cloning and Expression of Rat Liver and
;    TITLE OF INVENTION:  Porcine Liver Ribonuclease Inhibitor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,395
;      FILING DATE:  04-FEB-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1371 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1368
US-08-795-395-1

  Query Match             4.6%;  Score 183.8;  DB 2;  Length 1371;
  Best Local Similarity   47.2%;  Pred. No. 7e-44;
  Matches  591;  Conservative    0;  Mismatches  657;  Indels    3;  Gaps    1;

. Qy       2016 CCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCG 2075

Db        102 CCTCACGGAGGAGCACTGCAAGGACATCGGTTCTGCCCTCCGGGCCAACCCCTCCCTGAC 161

Qy       2076 GCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAA 2135

Db        162 CGAGCTCTGCCTCCGCACCAACGAGCTGGGCGATGCCGGCGTGCACCTGGTGCTGCAGGG 221

Qy       2136 GCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCC- 2194

Db        222 CCTGCAGAGCCCCACCTGCAAGATCCAGAAGCTCAGCCTGCAGAACTGCTCCCTGACCGA 281

Qy       2195 --CTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAA 2252

Db        282 GGCGGGCTGCGGGGTCCTGCCCAGCACGCTGCGCTCCCTGCCCACGCTGCGGGAGCTGCA 341

Qy       2253 CTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACA 2312

Db        342 TCTCAGCGACAACCCACTGGGGGACGCCGGCCTGCGGCTGCTCTGTGAGGGGCTCCTGGA 401

Qy       2313 CCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTA 2372

Db        402 CCCCCAGTGCCACCTGGAGAAGCTGCAGTTGGAGTACTGCCGCCTGACGGCCGCCAGCTG 461

Qy       2373 CCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGG 2432

Db        462 CGAGCCCCTGGCCTCGGTGCTCAGGGCCACGCGGGCCTTGAAGGAGCTCACGGTGAGCAA 521

Qy       2433 AAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTG 2492

Db        522 CAACGACATCGGCGAGGCCGGCGCCCGGGTGCTGGGCCAGGGTCTGGCAGACTCTGCCTG 581

Qy       2493 CGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCT 2552

Db        582 CCAGCTGGAGACGCTCAGGCTGGAGAACTGCGGTCTCACGCCAGCCAACTGCAAAGACCT 641

Qy       2553 GGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCT 2612

Db        642 GTGCGGAATTGTGGCCTCCCAGGCCTCGCTGAGGGAGCTTGACCTGGGCAGCAACGGGCT 701

Qy       2613 GGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCA 2672

Db        702 GGGCGACGCGGGCATAGCCGAGCTGTGCCCCGGGCTCTTGAGCCCCGCCTCCCGCCTCAA 761

Qy       2673 GAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGC 2732

Db        762 GACCCTGTGGCTCTGGGAGTGTGACATCACCGCCAGTGGCTGCAGAGACCTCTGCCGTGT 821

Qy       2733 GCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAA 2792

Db        822 CCTCCAGGCCAAGGAGACCCTGAAGGAGCTCAGTCTGGCGGGCAACAAGCTGGGCGACGA 881

Qy       2793 TGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGA 2852

Db        882 GGGCGCCCGGCTGCTGTGCGAGAGCCTGCTGCAGCCCGGCTGCCAGCTGGAGTCCCTGTG 941

Qy       2853 GTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAG 2912

Db        942 GGTGAAGTCCTGCAGCCTCACGGCGGCCTGCTGCCAGCACGTCAGCTTGATGCTGACCCA 1001

Qy       2913 GAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGC 2972

Db       1002 GAACAAGCATCTCCTGGAACTTCAGTTGAGCAGCAACAAGCTGGGTGACTCTGGCATCCA 1061

Qy       2973 TGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGC 3032

Db       1062 GGAGCTGTGCCAGGCCCTGAGCCAGCCGGGCACCACACTGCGGGTGCTCTGTCTTGGGGA 1121

Qy       3033 ATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCA 3092

Db       1122 CTGTGAGGTGACCAACAGCGGCTGCAGCAGCCTCGCCTCGCTCCTGCTGGCCAACCGCAG 1181

Qy       3093 TCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTG 3152

Db       1182 CCTGCGAGAGCTGGACCTGAGCAACAACTGTGTGGGCGACCCGGGCGTCCTGCAGCTGCT 1241

Qy       3153 TTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTA 3212

Db       1242 GGGGAGCCTGGAGCAGCCGGGCTGCGCCCTGGAGCAGCTGGTCCTGTACGACACCTACTG 1301

Qy       3213 CCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCG 3263

Db       1302 GACGGAGGAGGTGGAGGACCGCCTGCAGGCCCTGGAGGGGAGCAAGCCCGG 1352
```

```
Db       1182 CCTGCGAGAGCTGGACCTGAGCAACAACTGTGTGGGCGACCCGGGCGTCCTGCAGCTGCT 1241

Qy       3153 TTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTA 3212

Db       1242 GGGGAGCCTGGAGCAGCCGGGCTGCGCCCTGGAGCAGCTGGTCCTGTACGACACCTACTG 1301

Qy       3213 CCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCG 3263

Db       1302 GACGGAGGAGGTGGAGGACCGCCTGCAGGCCCTGGAGGGGAGCAAGCCCGG 1352


RESULT 8
US-08-910-731-5
; Sequence 5, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1386 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-910-731-5

  Query Match             4.5%;  Score 182.4;  DB 2;  Length 1386;
  Best Local Similarity   47.1%;  Pred. No. 1.9e-43;
  Matches  595;  Conservative    0;  Mismatches  666;  Indels    3;  Gaps    1;

Qy       2000 GGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCA 2059

Db        101 GGCTGGACGACTGTGGCCTCACGGAAGCACGGTGCAAGGACATCAGCTCTGCACTTCGAG 160

Qy       2060 CCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGA 2119

Db        161 TCAACCCTGCACTGGCAGAGCTCAACCTGCGCAGCAACGAGCTGGGCGATGTCGGCGTGC 220

Qy       2120 AGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGAA 2179

Db        221 ATTGCGTGCTCCAGGGCCTGCAGACCCCCTCCTGCAAGATCCAGAAGCTGAGCCTCCAGA 280

Qy       2180 ATGCACAGATTACCC---CTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTA 2236

Db        281 ACTGCTGCCTGACGGGGGCCGGCTGCGGGGTCCTGTCCAGCACACTACGCACCCTGCCCA 340

Qy       2237 ACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGT 2296

Db        341 CCCTGCAGGAGCTGCACCTCAGCGACAACCTCTTGGGGGATGCGGGCCTGCAGCTGCTCT 400

Qy       2297 GTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGAT 2356

Db        401 GCGAAGGACTCCTGGACCCCCAGTGCCGCCTGGAAAAGCTGCAGCTGGAGTATTGCAGCC 460

Qy       2357 TGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAAT 2416

Db        461 TCTCGGCTGCCAGCTGCGAGCCCCTGGCCTCCGTGCTCAGGGCCAAGCCGGACTTCAAGG 520

Qy       2417 CTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCT 2476

Db        521 AGCTCACGGTTAGCAACAACGACATCAATGAGGCTGGCGTCCGTGTGCTGTGCCAGGGCC 580

Qy       2477 TGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCA 2536

Db        581 TGAAGGACTCCCCCTGCCAGCTGGAGGCGCTCAAGCTGGAGAGCTGCGGTGTGACATCAG 640

Qy       2537 CGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCC 2596

Db        641 ACAACTGCCGGGACCTGTGCGGCATTGTGGCCTCCAAGGCCTCGCTGCGGGAGCTGGCCC 700

Qy       2597 TATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTC 2656

Db        701 TGGGCAGCAACAAGCTGGGTGATGTGGGCATGGCGGAGCTGTGCCCAGGGCTGCTCCACC 760

Qy       2657 CCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTG 2716

Db        761 CCAGCTCCAGGCTCAGGACCCTGTGGATCTGGGAGTGTGGCATCACTGCCAAGGGCTGCG 820

Qy       2717 GTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGA 2776

Db        821 GGGATCTGTGCCGTGTCCTCAGGGCCAAGGAGAGCCTGAAGGAGCTCAGCCTGGCCGGCA 880

Qy       2777 ACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTC 2836

Db        881 ACGAGCTGGGGGATGAGGGTGCCCGACTGCTGTGTGAGACCCTGCTGGAACCTGGCTGCC 940

Qy       2837 ATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGT 2896

Db        941 AGCTGGAGTCGCTGTGGGTGAAGTCCTGCAGCTTCACAGCCGCCTGCTGCCCCCACTTCA 1000

Qy       2897 CCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGG 2956

Db       1001 GCTCAGTGCTGGCCCAGAACAGGTTTCTCCTGGAGCTACAGATAAGCAACAACAGGCTGG 1060

Qy       2957 GTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGA 3016

Db       1061 AGGATGCGGGCGTGCGGGAGCTGTGCCAGGGCCTGGGCCAGCCTGGCTCTGTGCTGCGGG 1120

Qy       3017 GACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCC 3076

Db       1121 TGCTCTGGTTGGCCGACTGCGATGTGAGTGACAGCAGCTGCAGCAGCCTCGCCGCAACCC 1180

Qy       3077 TTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAG 3136

Db       1181 TGTTGGCCAACCACAGCCTGCGTGAGCTGGACCTCAGCAACAACTGCCTGGGGGACGCCG 1240

Qy       3137 GAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGC 3196

Db       1241 GCATCCTGCAGCTGGTGGAGAGCGTCCGGCAGCCGGGCTGCCTCCTGGAGCAGCTGGTCC 1300

Qy       3197 TGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCA 3256
```

```
Db       1301 TGTACGACATTTACTGGTCTGAGGAGATGGAGGACCGGCTGCAGGCCCTGGAGAAGGACA 1360

Qy       3257 AGCC 3260
Db       1361 AGCC 1364


RESULT 9
US-08-910-731-7
; Sequence 7, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1371 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-910-731-7

  Query Match             4.5%;  Score 180.8;  DB 2;  Length 1371;
  Best Local Similarity   47.1%;  Pred. No. 5.5e-43;
  Matches  588;  Conservative    0;  Mismatches  657;  Indels    3;  Gaps    1;

Qy       2016 CCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCG 2075
Db        102 CCTCACGGAGGAGCACTGCAAGGACATCGGTTCTGCCCTCCGGGCCAACCCCTCCCTGAC 161

Qy       2076 GCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAA 2135
Db        162 CGAGCTCTGCCTCCGCACCAACGAGCTGGGCGATGCCGGCGTGCACCTGGTGCTGCAGGG 221

Qy       2136 GCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCC- 2194
Db        222 CCTGCAGAGCCCCACCTGCAAGATCCAGAAGCTCAGCCTGCAGAACTGCTCCCTGACCGA 281

Qy       2195 --CTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAA 2252
Db        282 GGCGGGCTGCGGGGTCCTGCCCAGCACGCTGCGCTCCCTGCCCACGCTGCGGGAGCTGCA 341

Qy       2253 CTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACA 2312
Db        342 TCTCAGCGACAACCCACTGGGGGACGCCGGCCTGCGGCTGCTCTGTGAGGGGCTCCTGGA 401

Qy       2313 CCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTA 2372
Db        402 CCCCCAGTGCCACCTGGAGAAGCTGCAGTTGGAGTACTGCCGCCTGACGGCCGCCAGCTG 461

Qy       2373 CCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGG 2432
Db        462 CGAGCCCCTGGCCTCGGTGCTCAGGGCCACGCGGGCCTTGAAGGAGCTCACGGTGAGCAA 521

Qy       2433 AAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTG 2492
Db        522 CAACGACATCGGCGAGGCCGGCGCCCGGGTGCTGGGCCAGGGTCTGGCCGACTCTGCCTG 581

Qy       2493 CGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCT 2552
Db        582 CCAGCTGGAGACGCTCAGGCTGGAGAACTGCGGTCTCACGCCAGCCAACTGCAAAGACCT 641

Qy       2553 GGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCT 2612
Db        642 GTGCGGAATTGTGGCCTCCCAGGCCTCGCTGCGGGAGCTGGCCCTGGGCAGCAACAAGCT 701

Qy       2613 GGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCA 2672
Db        702 GGGTGATGTGGGCATGGCGGAGCTGTGCCCAGGGCTGCTCCACCCCAGCTCCAGGCTCAG 761

Qy       2673 GAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGC 2732
Db        762 GACCCTGTGGATCTGGGAGTGTGGCATCACTGCCAAGGGCTGCGGGGATCTGTGCCGTGT 821

Qy       2733 GCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAA 2792
Db        822 CCTCAGGGCCAAGGAGAGCCTGAAGGAGCTCAGCCTGGCCGGCAACGAGCTGGGGGATGA 881

Qy       2793 TGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGA 2852
Db        882 GGGTGCCCGACTGCTGTGTGAGACCCTGCTGGAACCTGGCTGCCAGCTGGAGTCGCTGTG 941

Qy       2853 GTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAG 2912
Db        942 GGTGAAGTCCTGCAGCTTCACAGCCGCCTGCTGCCCCCACTTCAGCTCAGTGCTGGCCCA 1001

Qy       2913 GAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGC 2972
Db       1002 GAACAGGTTTCTCCTGGAGCTACAGATAAGCAACAACAGGCTGGAGGATGCGGGCGTGCG 1061

Qy       2973 TGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGC 3032
Db       1062 GGAGCTGTGCCAGGGCCTGGGCCAGCCTGGCTCTGTGCTGCGGGTGCTCTGGTTGGCCGA 1121

Qy       3033 ATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCA 3092
Db       1122 CTGCGATGTGAGTGACAGCAGCTGCAGCAGCCTCGCCGCAACCCTGTTGGCCAACCACAG 1181

Qy       3093 TCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTG 3152
Db       1182 CCTGCGTGAGCTGGACCTCAGCAACAACTGCCTGGGGGACGCCGGCATCCTGCAGCTGGT 1241

Qy       3153 TTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTA 3212
Db       1242 GGAGAGCGTCCGGCAGCCGGGCTGCCTCCTGGAGCAGCTGGTCCTGTACGACATTTACTG 1301

Qy       3213 CCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCC 3260
Db       1302 GTCTGAGGAGATGGAGGACCGGCTGCAGGCCCTGGAGAAGGACAAGCC 1349
```

```
RESULT 10
US-08-910-731-3
; Sequence 3, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1374 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1368
US-08-910-731-3

  Query Match             4.4%;  Score 175.8;  DB 2;  Length 1374;
  Best Local Similarity   47.2%;  Pred. No. 1.7e-41;
  Matches  568;  Conservative    0;  Mismatches  632;  Indels    3;  Gaps    1;

Qy       2000 GGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCA 2059
Db         86 GGCTGGATGACTGTGGCCTCACTGAAGTGCGGTGCAAAGACATCAGGTCAGCGATCCAGG 145

Qy       2060 CCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGA 2119
Db        146 CCAACCCTGCCCTGACAGAGCTCAGCCTACGCACCAATGAACTGGGTGATGCTGGTGTGG 205

Qy       2120 AGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGAA 2179
Db        206 GTCTGGTGCTCCAGGGCCTGCAGAATCCCACTTGTAAGATCCAGAAGCTGAGCCTTCAGA 265

Qy       2180 ATGCACAGATTACCC---CTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTA 2236
Db        266 ACTGCAGCTTGACGGAAGCTGGCTGTGGGGTCCTGCCTGATGTGCTGCGCTCTTTGTCTA 325

Qy       2237 ACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGT 2296
Db        326 CCCTGCGTGAACTACATCTCAATGACAACCCTCTGGGGGATGAAGGCCTGAAGCTGCTCT 385

Qy       2297 GTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGAT 2356
Db        386 GTGAAGGACTCCGGGACCCCCAGTGCCGTCTTGAGAAGCTTCAGTTGGAATACTGTAACC 445

Qy       2357 TGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAAT 2416
Db        446 TCACAGCTACCAGCTGCGAGCCCCTGGCCTCAGTGCTCAGGGTGAAACCTGACTTTAAAG 505

Qy       2417 CTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCT 2476
Db        506 AGCTAGTATTGAGCAACAATGACTTCCATGAGGCTGGTATCCACACTCTGTGCCAGGGCC 565

Qy       2477 TGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCA 2536
Db        566 TGAAGGATTCTGCCTGTCAACTGGAGTCACTCAAACTGGAGAACTGTGGTATCACATCAG 625

Qy       2537 CGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCC 2596
Db        626 CCAACTGCAAGGATCTGTGTGATGTTGTGGCCTCCAAAGCCTCACTGCAAGAACTGGACT 685

Qy       2597 TATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTC 2656
Db        686 TGGGCAGCAACAAGCTGGGCAACACAGGCATTGCAGCACTGTGCTCAGGACTGCTGCTTC 745

Qy       2657 CCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTG 2716
Db        746 CCAGCTGCAGGCTGAGGACTCTGTGGCTCTGGGACTGTGATGTCACTGCAGAAGGCTGCA 805

Qy       2717 GTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGA 2776
Db        806 AGGACCTGTGCCGTGTCCTCAGAGCCAAGCAGAGCCTGAAGGAACTCAGCCTAGCTGGCA 865

Qy       2777 ACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTC 2836
Db        866 ATGAGCTGAAGGATGAGGGTGCCCAACTGCTGTGTGAGAGCCTGTTAGAGCCTGGCTGTC 925

Qy       2837 ATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGT 2896
Db        926 AGCTGGAGTCACTGTGGGTAAAGACCTGTAGCCTCACAGCTGCCTCTTGTCCCCACTTCT 985

Qy       2897 CCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGG 2956
Db        986 GCTCGGTGTTGACCAAAAACAGTTCTCTGTTTGAGTTGCAAATGAGCAGCAACCCGCTGG 1045

Qy       2957 GTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGA 3016
Db       1046 GAGACTCGGGAGTCGTGGAGCTTTGCAAGGCCCTGGGCTATCCGGACACAGTGCTGCGTG 1105

Qy       3017 GACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCC 3076
Db       1106 TGCTTTGGCTGGGAGACTGTGATGTGACAGACAGTGGCTGCAGCAGCCTTGCCACTGTCC 1165

Qy       3077 TTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAG 3136
Db       1166 TGCTGGCCAACCGCAGCTTGAGGGAACTGGACCTCAGTAACAACTGCATGGGGGACAACG 1225

Qy       3137 GAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGC 3196
Db       1226 GTGTCCTACAACTGCTGGAGAGCCTCAAACAGCCCAGCTGCATCCTTCAGCAGCTTGTCC 1285

Qy       3197 TGT 3199
Db       1286 TGT 1288

RESULT 11
US-08-795-395-3
; Sequence 3, Application US/08795395
```

```
; Patent No. 5965399
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Cloning and Expression of Rat Liver and
;    TITLE OF INVENTION:  Porcine Liver Ribonuclease Inhibitor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,395
;      FILING DATE:  04-FEB-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1374 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1368
US-08-795-395-3

  Query Match             4.4%;  Score 175.8;  DB 2;  Length 1374;
  Best Local Similarity   47.2%;  Pred. No. 1.7e-41;
  Matches  568;  Conservative    0;  Mismatches  632;  Indels    3;  Gaps    1;

Qy       2000 GGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCA 2059
Db         86 GGCTGGATGACTGTGGCCTCACTGAAGTGCGGTGCAAAGACATCAGGTCAGCGATCCAGG 145

Qy       2060 CCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGA 2119
Db        146 CCAACCCTGCCCTGACAGAGCTCAGCCTACGCACCAATGAACTGGGTGATGCTGGTGTGG 205

Qy       2120 AGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGAA 2179
Db        206 GTCTGGTGCTCCAGGGCCTGCAGAATCCCACTTGTAAGATCCAGAAGCTGAGCCTTCAGA 265

Qy       2180 ATGCACAGATTACCC---CTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTA 2236
Db        266 ACTGCAGCTTGACGGAAGCTGGCTGTGGGGTCCTGCCTGATGTGCTGCGCTCTTTGTCTA 325

Qy       2237 ACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGT 2296
Db        326 CCCTGCGTGAACTACATCTCAATGACAACCCTCTGGGGGATGAAGGCCTGAAGCTGCTCT 385

Qy       2297 GTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGAT 2356
Db        386 GTGAAGGACTCCGGGACCCCCAGTGCCGTCTTGAGAAGCTTCAGTTGGAATACTGTAACC 445

Qy       2357 TGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAAT 2416
Db         446 TCACAGCTACCAGCTGCGAGCCCCTGGCCTCAGTGCTCAGGGTGAAACCTGACTTTAAAG 505

Qy       2417 CTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCT 2476
Db         506 AGCTAGTATTGAGCAACAATGACTTCCATGAGGCTGGTATCCACACTCTGTGCCAGGGCC 565

Qy       2477 TGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCA 2536
Db         566 TGAAGGATTCTGCCTGTCAACTGGAGTCACTCAAACTGGAGAACTGTGGTATCACATCAG 625

Qy       2537 CGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCC 2596
Db         626 CCAACTGCAAGGATCTGTGTGATGTTGTGGCCTCCAAAGCCTCACTGCAAGAACTGGACT 685

Qy       2597 TATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTC 2656
Db         686 TGGGCAGCAACAAGCTGGGCAACACAGGCATTGCAGCACTGTGCTCAGGACTGCTGCTTC 745

Qy       2657 CCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTG 2716
Db         746 CCAGCTGCAGGCTGAGGACTCTGTGGCTCTGGGACTGTGATGTCACTGCAGAAGGCTGCA 805

Qy       2717 GTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGA 2776
Db         806 AGGACCTGTGCCGTGTCCTCAGAGCCAAGCAGAGCCTGAAGGAACTCAGCCTAGCTGGCA 865

Qy       2777 ACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTC 2836
Db         866 ATGAGCTGAAGGATGAGGGTGCCCAACTGCTGTGTGAGAGCCTGTTAGAGCCTGGCTGTC 925

Qy       2837 ATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGT 2896
Db         926 AGCTGGAGTCACTGTGGGTAAAGACCTGTAGCCTCACAGCTGCCTCTTGTCCCCACTTCT 985

Qy       2897 CCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGG 2956
Db         986 GCTCGGTGTTGACCAAAAACAGTTCTCTGTTTGAGTTGCAAATGAGCAGCAACCCGCTGG 1045

Qy       2957 GTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGA 3016
Db        1046 GAGACTCGGGAGTCGTGGAGCTTTGCAAGGCCCTGGGCTATCCGGACACAGTGCTGCGTG 1105

Qy       3017 GACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCC 3076
Db        1106 TGCTTTGGCTGGGAGACTGTGATGTGACAGACAGTGGCTGCAGCAGCCTTGCCACTGTCC 1165

Qy       3077 TTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAG 3136
Db        1166 TGCTGGCCAACCGCAGCTTGAGGGAACTGGACCTCAGTAACAACTGCATGGGGGACAACG 1225

Qy       3137 GAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGC 3196
Db        1226 GTGTCCTACAACTGCTGGAGAGCCTCAAACAGCCCAGCTGCATCCTTCAGCAGCTTGTCC 1285

Qy       3197 TGT 3199
Db        1286 TGT 1288


RESULT 12
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
```

```
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-Fls
US-08-232-463-14

  Query Match             1.5%;  Score 61;  DB 1;  Length 7218;
  Best Local Similarity   1.1%;  Pred. No. 1.2e-06;
  Matches    4;  Conservative  225;  Mismatches  130;  Indels    0;  Gaps    0;

Qy        264 GGAGAAGGCACGGGATGACATGAAAAAAATTTCACAAGCTATGGAACAAGAAGGTGCCAC 323
              :::::::: : :::: :: : ::::::::    : :::  : :::: :::::::: :  :
Db       1421 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1362

Qy        324 AGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGC 383
              :: :: :::: ::::::: ::::::    : :::  : :::: ::::::: :  : ::
Db       1361 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1302

Qy        384 AGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGTCACGTGAT 443
              :: ::::: ::::::: ::::: : ::::: :: : : ::::  : :::::  : : ::
Db       1301 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1242

Qy        444 GACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTG 503
              ::  :::   :  :::::::::::: : : :  : ::   ::::: :  :  :  ::  :
Db       1241 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1182

Qy        504 GCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCG 563
              :  ::::: : ::: :  ::  :: :     ::   :::  :: ::::     ::    :
Db       1181 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1122

Qy        564 CACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCG 622
              : :: ::    : : :::::  :::::  ::::::  ::    ::  ::::::||||
Db       1121 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRATCG 1063


RESULT 13
US-09-023-655-395
; Sequence 395, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  395:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  376 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  THP1PLB02
;      CLONE:  153338
US-09-023-655-395

  Query Match             1.5%;  Score 60;  DB 4;  Length 376;
  Best Local Similarity   55.6%;  Pred. No. 3e-07;
  Matches  134;  Conservative    0;  Mismatches  106;  Indels    1;  Gaps    1;

Qy       2914 AGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCT 2973
              | ||||  |  |  |  ||||| || |  ||||| ||||| ||||||   ||  |
Db         35 ACCAGAAGCTGGTTGGAGCTGGACCTGAGTGACAACGCCCTCGGTGACTTCGGAATCAGA 94

Qy       2974 GCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCA 3033
                ||||| | |||||||||||||    |     |  |||||  ||  ||| |||||
Db         95 CTTCTGTGTGTGGGACTGAAGCACCTGTTGTGCAATCTGAAGAAGCTCTGGTTGGTCAGC 154

Qy       3034 TGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCAT 3093
              ||  | || || || |  || ||| |||  ||  | |  |    |   |  || ||
Db        155 TGCTGCCTCACATCAGCATGTTGTCAGGATCTTNCATCAGTATTGAGCACCAGCCATTCC 214

Qy       3094 CTGACCAG-TCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTG 3152
              |||||||  ||  | ||| | |||||  |||  |   |  ||||  |     |  ||
Db        215 CTGACCAGACCTCTATGTGGGGGAGAATGCCTTGGGAGACTCAGGAGTCGCAATTTTATG 274

Qy       3153 T 3153
              |
Db        275 T 275


RESULT 14
US-09-949-016-16600
; Sequence 16600, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
```

```
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16600
;   LENGTH: 298336
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(298336)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16600

  Query Match             1.3%;  Score 51.4;  DB 4;  Length 298336;
  Best Local Similarity   58.0%;  Pred. No. 0.011;
  Matches   91;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

Qy       3273 TGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACACAAAATAGGACTTACTTTCCG 3332
              | |  | |  ||  ||| |||          |||    ||||||  |||       |||||
Db     202167 TTAGAGAATGTGTGATTATTTATTCATTCATGCAGTACACAAGGTAGTTTGGCATTTCCC 202226

Qy       3333 GCTCCCTGAAAGCCGGGCATGGCCATGTGCCTTGCTGTGGGGGATGAACCCAGAGCAGAA 3392
                ||  ||  |      |||| |||||||  |||||| |||   ||||| |  ||  ||||
Db     202227 ATTCTCTATACATTAAGCATAGCCATGTAACTTGCTCTGGTCAATGAATCATGAAAAGAA 202286

Qy       3393 GAAGCGTGTGTCGCTTCTGGCTGGAGACTTCAAGAGC 3429
              ||    | |||| | |||||  |||  ||| ||||||
Db     202287 GATATATATGTCACATCTGGGAGGAAGCTTTAAGAGC 202323


RESULT 15
US-09-949-016-14581/c
; Sequence 14581, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14581
;   LENGTH: 64309
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(64309)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14581

  Query Match             1.3%;  Score 50.8;  DB 4;  Length 64309;
  Best Local Similarity   58.7%;  Pred. No. 0.0059;
  Matches   88;  Conservative    0;  Mismatches   62;  Indels    0;  Gaps    0;

Qy        264 GGAGAAGGCACGGGATGACATGAAAAAAATTTCACAAGCTATGGAACAAGAAGGTGCCAC 323
              |||  ||| |  ||| ||   | || ||     | |||      ||| ||||||  |
Db      24025 GGAAGAGGAAGAGGAAGAAGAGGAAGAAGAAGAAAAAGAAGAAGAAGAAGAAGAAGA 23966

Qy        324 AGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGC 383
              || || |||   ||||||| |||||     | |||      ||| ||||||| |    ||
Db      23965 AGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGGAGAAGAAGA 23906

Qy        384 AGCAGAGACAGAAGAACAAGGACATGGAGG 413
              || |||   ||||||| ||| | | | |||
Db      23905 AGAAGAAGGAGAAGAAGAAGAAGAAGG 23876


Search completed: February  4, 2005, 13:21:15
Job time : 652 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 12:28:54 ; Search time 2017 Seconds
(without alignments)
11514.338 Million cell updates/sec

Title: US-10-066-521-5
Perfect score: 4035
Sequence: 1 atggaaggagacaaatcgct.....tcgaggggctggtgtcttaa 4035

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

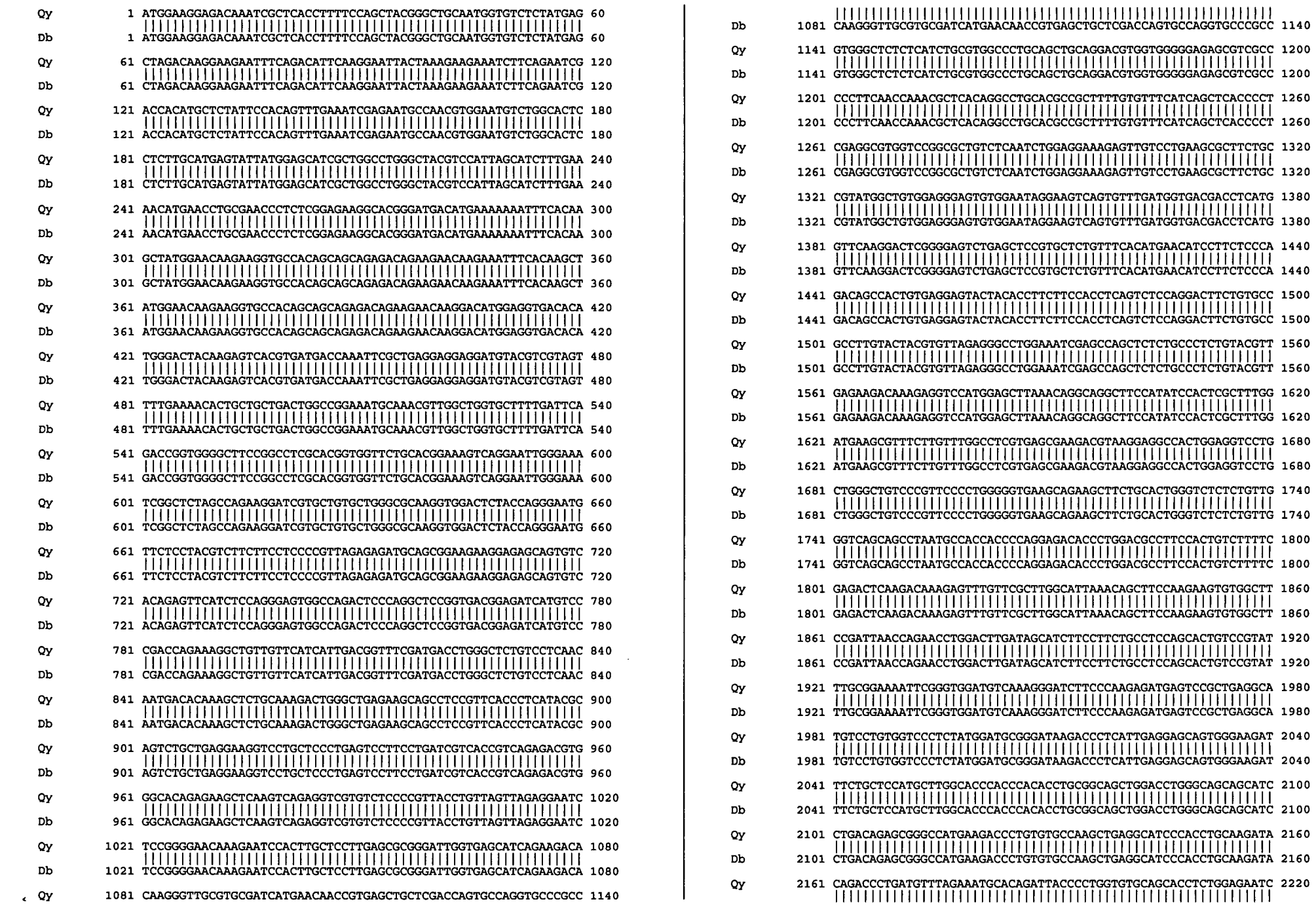
SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4035	100.0	4035	14	US-10-124-498-5	Sequence 5, Appli
2	4035	100.0	4035	14	US-10-066-521-5	Sequence 5, Appli
3	3166.2	78.5	3885	18	US-10-860-761-3	Sequence 3, Appli
4	3166.2	78.5	3900	17	US-10-399-443-23	Sequence 23, Appl
5	3166.2	78.5	3900	17	US-10-677-943-23	Sequence 23, Appl
6	3139	77.8	3830	15	US-10-216-645-3	Sequence 3, Appli
7	3133.6	77.7	3489	17	US-10-416-642-3	Sequence 3, Appli
8	3133.6	77.7	3926	15	US-10-216-645-1	Sequence 1, Appli
9	2900.6	71.9	3226	17	US-10-092-900A-347	Sequence 347, App
10	1278	31.7	3447	17	US-10-399-443-5	Sequence 5, Appli
11	1278	31.7	3447	17	US-10-677-943-5	Sequence 5, Appli
12	1152.8	28.6	1157	17	US-10-399-443-1	Sequence 1, Appli
13	1152.8	28.6	1157	17	US-10-677-943-1	Sequence 1, Appli
14	756.6	18.8	1075	17	US-10-399-443-3	Sequence 3, Appli
15	756.6	18.8	1075	17	US-10-677-943-3	Sequence 3, Appli
16	729.4	18.1	3521	18	US-10-794-342-2	Sequence 2, Appli
17	438	10.9	2775	17	US-10-357-820-51	Sequence 51, Appl
18	424	10.5	2985	10	US-09-965-621-15	Sequence 15, Appl
19	424	10.5	2985	17	US-10-407-866-15	Sequence 15, Appl
20	424	10.5	2985	18	US-10-781-294-15	Sequence 15, Appl
21	422.4	10.5	2982	14	US-10-124-498-25	Sequence 25, Appl
22	422.4	10.5	2982	14	US-10-066-521-25	Sequence 25, Appl
23	422.4	10.5	3190	17	US-10-094-749-1079	Sequence 1079, Ap
24	422.4	10.5	3368	14	US-10-124-498-23	Sequence 23, Appl
25	422.4	10.5	3368	14	US-10-066-521-23	Sequence 23, Appl
26	419.2	10.4	2575	9	US-09-848-035-7	Sequence 7, Appli
27	419.2	10.4	2575	9	US-09-986-224-7	Sequence 7, Appli
28	419.2	10.4	2883	17	US-10-161-493-3	Sequence 3, Appli
29	419.2	10.4	3172	18	US-10-398-037-74	Sequence 74, Appl
30	409	10.1	3186	14	US-10-124-498-17	Sequence 17, Appl
31	409	10.1	3186	14	US-10-066-521-17	Sequence 17, Appl
32	404.4	10.0	3108	10	US-09-965-621-23	Sequence 23, Appl
33	404.4	10.0	3108	17	US-10-407-866-23	Sequence 23, Appl
34	404.4	10.0	3108	18	US-10-781-294-23	Sequence 23, Appl
35	404.4	10.0	3218	17	US-10-407-866-67	Sequence 67, Appl
36	392.6	9.7	3189	15	US-10-239-663-10	Sequence 10, Appl
37	390.6	9.7	3540	18	US-10-794-342-7	Sequence 7, Appli
38	381.4	9.5	3099	13	US-10-127-516-3	Sequence 3, Appli
39	381.4	9.5	3099	13	US-10-027-629-3	Sequence 3, Appli
40	381.4	9.5	3099	16	US-10-132-967-3	Sequence 3, Appli
41	381.4	9.5	3431	13	US-10-127-516-1	Sequence 1, Appli
42	381.4	9.5	3431	13	US-10-027-629-1	Sequence 1, Appli
43	381.4	9.5	3431	16	US-10-132-967-1	Sequence 1, Appli
44	368.4	9.1	2763	18	US-10-250-615-39	Sequence 39, Appl
45	357.6	8.9	3466	17	US-10-108-260A-718	Sequence 718, App

ALIGNMENTS

RESULT 1
US-10-124-498-5
; Sequence 5, Application US/10124498
; Publication No. US20030017983A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-367001
; CURRENT APPLICATION NUMBER: US/10/124,498
; CURRENT FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 10/066,521
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4035
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4032)
US-10-124-498-5

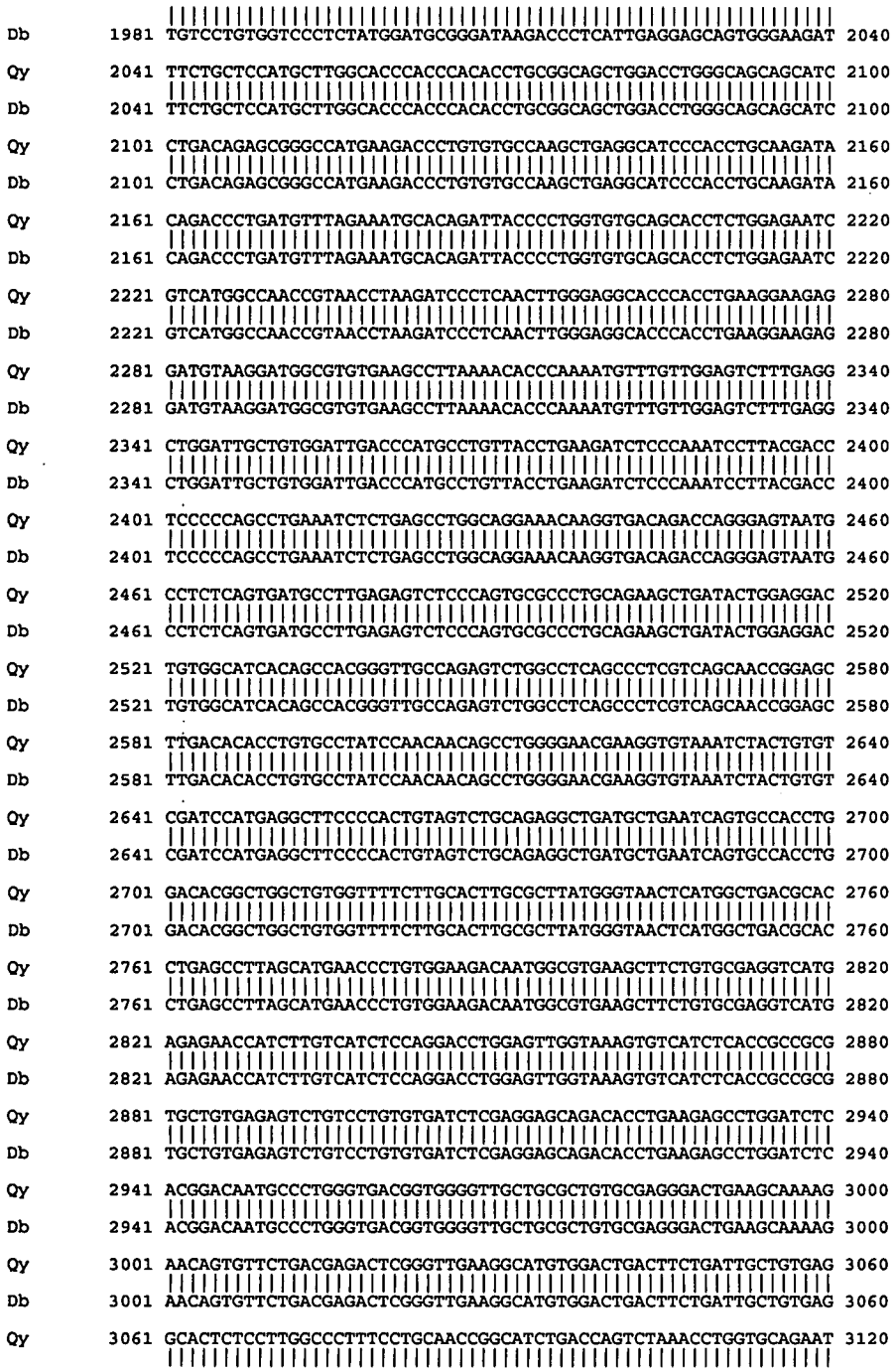
Query Match 100.0%; Score 4035; DB 14; Length 4035;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


Qy 1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
Db 1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
Qy 61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
Db 61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
Qy 121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
Db 121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
Qy 181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
Db 181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
Qy 241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300
Db 241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300
Qy 301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360
Db 301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360
Qy 361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420
Db 361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420
Qy 421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480
Db 421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480
Qy 481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540
Db 481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540
Qy 541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600
Db 541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600
Qy 601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660
Db 601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660
Qy 661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720
Db 661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720
Qy 721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780
Db 721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780
Qy 781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840
Db 781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840
Qy 841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900
Db 841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900
Qy 901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960
Db 901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960
Qy 961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020
Db 961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020
Qy 1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080
Db 1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080
Qy 1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140
Db 1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140
Qy 1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200
Db 1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200
Qy 1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260
Db 1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260
Qy 1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320
Db 1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320
Qy 1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380
Db 1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380
Qy 1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440
Db 1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440
Qy 1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500
Db 1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500
Qy 1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560
Db 1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560
Qy 1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620
Db 1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620
Qy 1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680
Db 1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680
Qy 1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740
Db 1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740
Qy 1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800
Db 1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800
Qy 1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860
Db 1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860
Qy 1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920
Db 1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920
Qy 1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980
Db 1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980
Qy 1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040
Db 1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040
Qy 2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100
Db 2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100
Qy 2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160
Db 2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160
Qy 2161 CAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATC 2220

```
Db       2161 CAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATC 2220
Qy       2221 GTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 GTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAG 2280
Qy       2281 GATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGG 2340
Qy       2341 CTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 CTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACC 2400
Qy       2401 TCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATG 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 TCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATG 2460
Qy       2461 CCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGAC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 CCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGAC 2520
Qy       2521 TGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGC 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGC 2580
Qy       2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640
Qy       2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700
Qy       2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760
Qy       2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820
Qy       2821 AGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCG 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 AGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCG 2880
Qy       2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940
Qy       2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000
Qy       3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060
Qy       3061 GCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAAT 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 GCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAAT 3120
Qy       3121 AACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAAC 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 AACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAAC 3180
Qy       3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240
Qy       3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300
Qy       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360
Qy       3361 GCCTTGCTGTGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GCCTTGCTGTGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420
Qy       3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480
Qy       3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540
Qy       3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600
Qy       3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660
Qy       3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720
Qy       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780
Qy       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840
Qy       3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900
Qy       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960
Qy       3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020
Qy       4021 GGGCTGGTGTCTTAA 4035
             |||||||||||||||
Db       4021 GGGCTGGTGTCTTAA 4035
```

RESULT 2
US-10-066-521-5
; Sequence 5, Application US/10066521
; Publication No. US20030027757A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-334001
; CURRENT APPLICATION NUMBER: US/10/066,521
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0

```
; SEQ ID NO 5
;   LENGTH: 4035
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(4032)
US-10-066-521-5

  Query Match            100.0%;  Score 4035;  DB 14;  Length 4035;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 4035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300

Qy        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360

Qy        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420

Qy        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480

Qy        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540

Qy        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600

Qy        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660

Qy        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720

Qy        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780

Qy        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840

Qy        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900

Qy        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960

Qy        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020

Qy       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080

Qy       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140

Qy       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200

Qy       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260

Qy       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320

Qy       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380

Qy       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440

Qy       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500

Qy       1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560

Qy       1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620

Qy       1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680

Qy       1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740

Qy       1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800

Qy       1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860

Qy       1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920

Qy       1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980

Qy       1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040
```



RESULT 3
US-10-860-761-3
; Sequence 3, Application US/10860761
; Publication No. US20040248775A1
; GENERAL INFORMATION:
; APPLICANT: WYETH

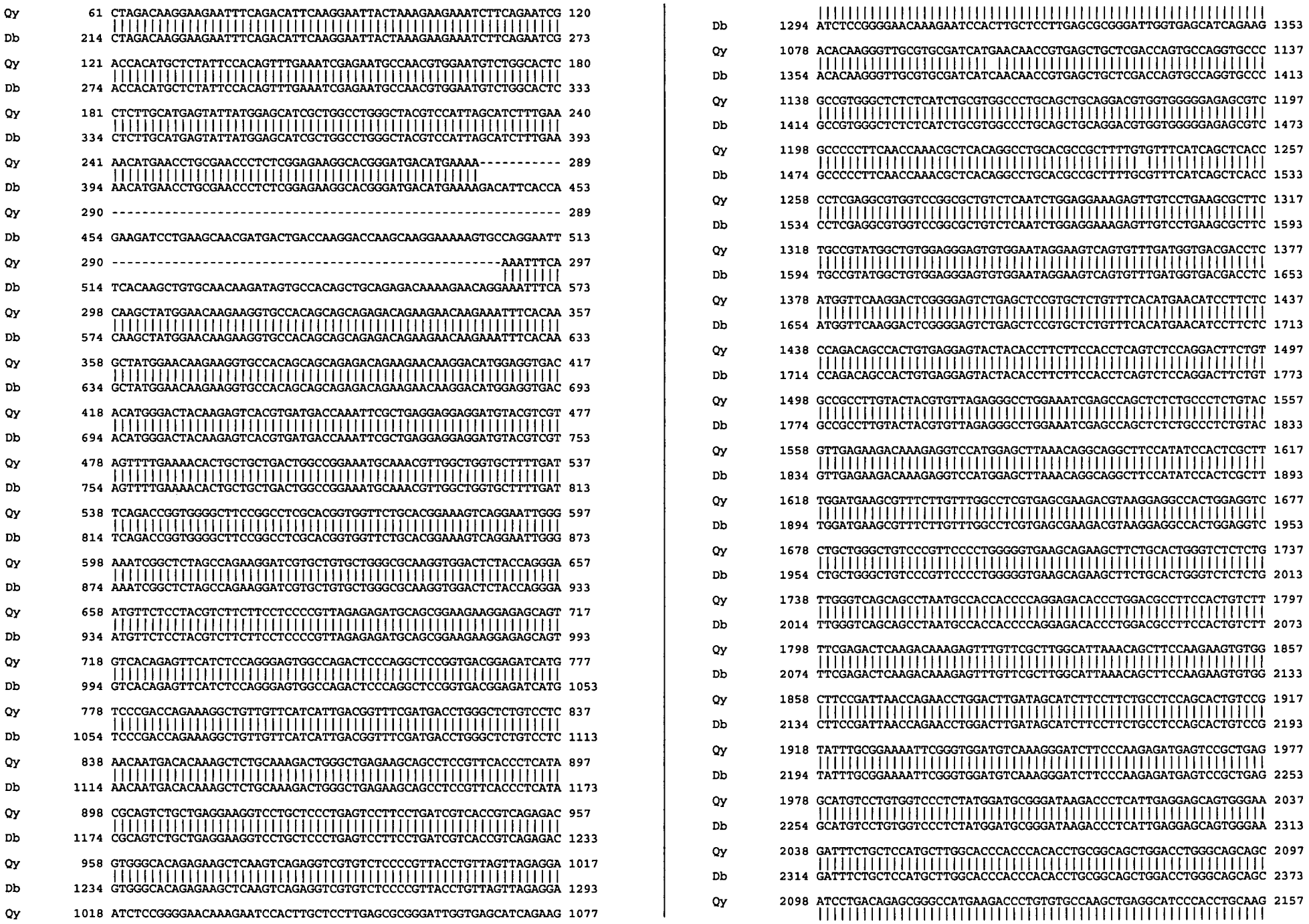
```
;  TITLE OF INVENTION: METHODS FOR SCREENING INHIBITORS OF APOPTOSIS
;  FILE REFERENCE: AM101318
;  CURRENT APPLICATION NUMBER: US/10/860,761
;  CURRENT FILING DATE:  2004-06-03
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 3885
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3603)
US-10-860-761-3

  Query Match            78.5%;  Score 3166.2;  DB 18;  Length 3885;
  Best Local Similarity  96.2%;  Pred. No. 0;
  Matches 3304;  Conservative    0;  Mismatches    8;  Indels  123;  Gaps    1;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 213

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 273

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 333

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 393

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAGACATTCACCA 453

Qy        290 ---------------------------------------------------------- 289

Db        454 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 513

Qy        290 ----------------------------------------------------AAATTTCA 297
                                                                   ||||||||
Db        514 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGAGACAAAAGAACAGGAAATTTCA 573

Qy        298 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 633

Qy        358 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 693

Qy        418 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 753

Qy        478 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 813

Qy        538 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 873

Qy        598 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 933

Qy        658 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        934 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 993

Qy        718 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 1053

Qy        778 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 1113

Qy        838 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 1173

Qy        898 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 1233

Qy        958 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1293

Qy       1018 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1077
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1353

Qy       1078 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 ACACAAGGGTTGCGTGCGATCATCAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1413

Qy       1138 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1473

Qy       1198 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACC 1257
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1474 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGCGTTTCATCAGCTCACC 1533

Qy       1258 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1593

Qy       1318 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1653

Qy       1378 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1713

Qy       1438 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1773

Qy       1498 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1833

Qy       1558 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1893

Qy       1618 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1677
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1953

Qy       1678 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 1737
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1954 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 2013

Qy       1738 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 1797
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2014 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 2073
```

```
Qy       1798 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 1857
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2074 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 2133

Qy       1858 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 1917
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2134 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 2193

Qy       1918 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 1977
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2194 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 2253

Qy       1978 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2037
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2254 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2313

Qy       2038 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2097
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2314 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2373

Qy       2098 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2157
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2374 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2433

Qy       2158 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 2217
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       2434 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACCTCTGGAGA 2493

Qy       2218 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2277
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2494 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2553

Qy       2278 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2337
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2554 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2613

Qy       2338 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2397
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2614 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2673

Qy       2398 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2733

Qy       2458 ATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2517
             | ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       2734 ACGCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2793

Qy       2518 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2794 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2853

Qy       2578 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2854 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2913

Qy       2638 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2914 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2973

Qy       2698 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 2757
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       2974 CTGGACACGGCTGGCTGTGGTTCTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 3033

Qy       2758 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 2817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3034 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 3093

Qy       2818 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 2877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3094 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 3153

Qy       2878 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 2937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 3213

Qy       2938 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 2997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3214 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 3273

Qy       2998 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3274 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3333

Qy       3058 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3334 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3393

Qy       3118 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3394 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3453

Qy       3178 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3237
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3454 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3513

Qy       3238 GAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGAT 3297
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3514 GAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGAT 3573

Qy       3298 GAAGATGACCGACAC 3312
             |||||||||| ||
Db       3574 GAAGATGACCGGTAC 3588
```

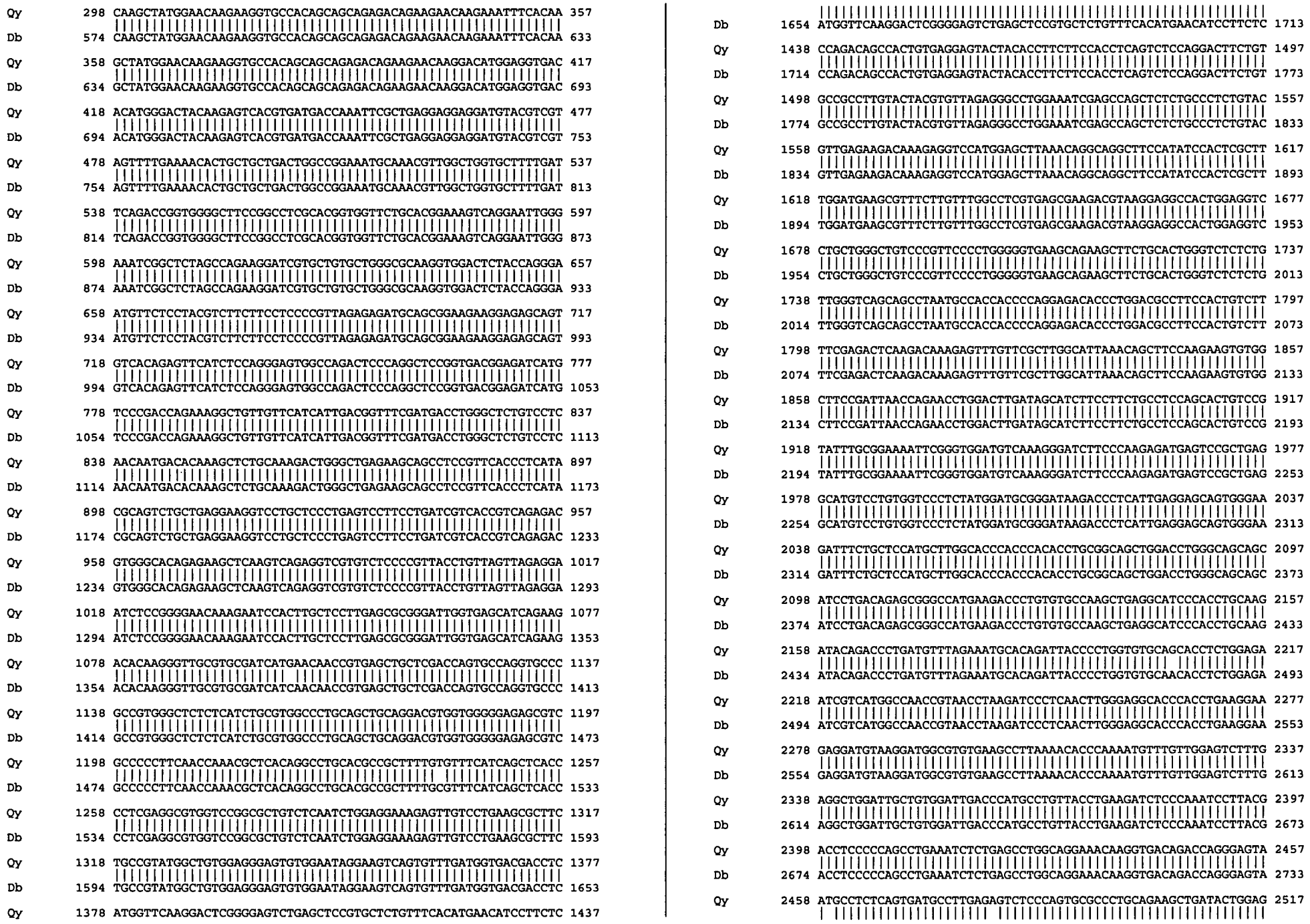
RESULT 4
US-10-399-443-23
; Sequence 23, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3600)
; OTHER INFORMATION:
US-10-399-443-23

Query Match 78.5%; Score 3166.2; DB 17; Length 3900;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 3304; Conservative 0; Mismatches 8; Indels 123; Gaps 1;

```
Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 213
```


Qy 61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
Db 214 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 273
Qy 121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
Db 274 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 333
Qy 181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
Db 334 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 393
Qy 241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
Db 394 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAGACATTCACCA 453
Qy 290 ---------- 289
Db 454 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 513
Qy 290 ----------AAATTTCA 297
Db 514 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGAGACAAAAGAACAGGAAATTTCA 573
Qy 298 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 357
Db 574 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 633
Qy 358 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 417
Db 634 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 693
Qy 418 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 477
Db 694 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 753
Qy 478 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 537
Db 754 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 813
Qy 538 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 597
Db 814 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 873
Qy 598 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 657
Db 874 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 933
Qy 658 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 717
Db 934 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 993
Qy 718 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 777
Db 994 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 1053
Qy 778 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 837
Db 1054 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 1113
Qy 838 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 897
Db 1114 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 1173
Qy 898 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 957
Db 1174 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 1233
Qy 958 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1017
Db 1234 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1293
Qy 1018 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1077
Db 1294 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1353
Qy 1078 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1137
Db 1354 ACACAAGGGTTGCGTGCGATCATCAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1413
Qy 1138 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1197
Db 1414 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1473
Qy 1198 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACC 1257
Db 1474 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGCGTTTCATCAGCTCACC 1533
Qy 1258 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1317
Db 1534 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1593
Qy 1318 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1377
Db 1594 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1653
Qy 1378 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1437
Db 1654 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1713
Qy 1438 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1497
Db 1714 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1773
Qy 1498 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1557
Db 1774 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1833
Qy 1558 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1617
Db 1834 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1893
Qy 1618 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1677
Db 1894 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1953
Qy 1678 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 1737
Db 1954 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 2013
Qy 1738 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 1797
Db 2014 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 2073
Qy 1798 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 1857
Db 2074 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 2133
Qy 1858 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 1917
Db 2134 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 2193
Qy 1918 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 1977
Db 2194 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 2253
Qy 1978 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2037
Db 2254 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2313
Qy 2038 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2097
Db 2314 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2373
Qy 2098 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2157

```
Db       2374 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2433

Qy       2158 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 2217
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       2434 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACCTCTGGAGA 2493

Qy       2218 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2494 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2553

Qy       2278 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2554 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2613

Qy       2338 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2614 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2673

Qy       2398 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2733

Qy       2458 ATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2517
              | |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       2734 ACGCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2793

Qy       2518 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2794 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2853

Qy       2578 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2854 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2913

Qy       2638 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2914 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2973

Qy       2698 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 2757
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       2974 CTGGACACGGCTGGCTGTGGTTCTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 3033

Qy       2758 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 2817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3034 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 3093

Qy       2818 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 2877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3094 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 3153

Qy       2878 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 2937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 3213

Qy       2938 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 2997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3214 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 3273

Qy       2998 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3274 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3333

Qy       3058 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3334 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3393

Qy       3118 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3394 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3453

Qy       3178 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3454 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3513

Qy       3238 GAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGAT 3297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3514 GAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGAT 3573

Qy       3298 GAAGATGACCGACAC 3312
              ||||||||||| ||
Db       3574 GAAGATGACCGGTAC 3588


RESULT 5
US-10-677-943-23
; Sequence 23, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
;   LENGTH: 3900
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3600)
US-10-677-943-23

  Query Match             78.5%;  Score 3166.2;  DB 17;  Length 3900;
  Best Local Similarity   96.2%;  Pred. No. 0;
  Matches 3304;  Conservative    0;  Mismatches    8;  Indels  123;  Gaps    1;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 213

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 273

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 333

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 393

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAGACATTCACCA 453

Qy        290 ---------------------------------------------------------- 289

Db        454 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 513

Qy        290 ----------------------------------------------------AAATTTCA 297
                                                                   ||||||||
Db        514 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGAGACAAAAGAACAGGAAATTTCA 573
```


Qy 298 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 357
Db 574 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 633
Qy 358 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 417
Db 634 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 693
Qy 418 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 477
Db 694 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 753
Qy 478 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 537
Db 754 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 813
Qy 538 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 597
Db 814 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 873
Qy 598 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 657
Db 874 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 933
Qy 658 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 717
Db 934 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 993
Qy 718 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 777
Db 994 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 1053
Qy 778 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 837
Db 1054 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 1113
Qy 838 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 897
Db 1114 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 1173
Qy 898 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 957
Db 1174 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 1233
Qy 958 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1017
Db 1234 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1293
Qy 1018 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1077
Db 1294 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1353
Qy 1078 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1137
Db 1354 ACACAAGGGTTGCGTGCGATCATCAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1413
Qy 1138 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1197
Db 1414 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1473
Qy 1198 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACC 1257
Db 1474 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGCGTTTCATCAGCTCACC 1533
Qy 1258 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1317
Db 1534 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1593
Qy 1318 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1377
Db 1594 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1653
Qy 1378 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1437
Db 1654 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1713
Qy 1438 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1497
Db 1714 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1773
Qy 1498 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1557
Db 1774 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1833
Qy 1558 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1617
Db 1834 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1893
Qy 1618 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1677
Db 1894 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1953
Qy 1678 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 1737
Db 1954 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 2013
Qy 1738 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 1797
Db 2014 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 2073
Qy 1798 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 1857
Db 2074 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 2133
Qy 1858 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 1917
Db 2134 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 2193
Qy 1918 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 1977
Db 2194 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 2253
Qy 1978 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2037
Db 2254 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2313
Qy 2038 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2097
Db 2314 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2373
Qy 2098 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2157
Db 2374 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2433
Qy 2158 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 2217
Db 2434 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACCTCTGGAGA 2493
Qy 2218 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2277
Db 2494 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2553
Qy 2278 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2337
Db 2554 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2613
Qy 2338 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2397
Db 2614 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2673
Qy 2398 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2457
Db 2674 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2733
Qy 2458 ATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2517

```
Db       2734 ACGCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2793

Qy       2518 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2794 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2853

Qy       2578 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2854 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2913

Qy       2638 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2914 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2973

Qy       2698 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 2757
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       2974 CTGGACACGGCTGGCTGTGGTTCTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 3033

Qy       2758 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 2817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3034 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 3093

Qy       2818 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 2877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3094 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 3153

Qy       2878 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 2937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 3213

Qy       2938 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 2997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3214 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 3273

Qy       2998 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3274 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3333

Qy       3058 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3334 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3393

Qy       3118 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3394 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3453

Qy       3178 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3237
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3454 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3513

Qy       3238 GAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGAT 3297
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3514 GAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGAT 3573

Qy       3298 GAAGATGACCGACAC 3312
             ||||||||||| ||
Db       3574 GAAGATGACCGGTAC 3588


RESULT 6
US-10-216-645-3
; Sequence 3, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
;  APPLICANT: WEISS, BERTRAM
;  APPLICANT:  LESSL, MONIKA
;  APPLICANT:  PETERS-KOTTIG, MICHAELE
;  APPLICANT:  BECKMANN, GEORG
;  TITLE OF INVENTION: HUMAN MATER PROTEINS
;  FILE REFERENCE: SCH-1910
;  CURRENT APPLICATION NUMBER: US/10/216,645
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 3830
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-216-645-3

  Query Match             77.8%;  Score 3139;  DB 15;  Length 3830;
  Best Local Similarity   96.0%;  Pred. No. 0;
  Matches 3282;  Conservative    0;  Mismatches   30;  Indels  105;  Gaps    2;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||      || ||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAATTCACCAGAA 300

Qy        301 GCT--------------ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACA- 344
              | ||              |  || |||| |     ||  | |  || | |||| | | |
Db        301 GATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGAAAATAAA 360

Qy        345 ------------------------------------------------------------ 344

Db        361 TATGGCATGACTAAGCTTATCTTGGGGGTGTCTGACATCTCTGACTCGAATAATAAACAC 420

Qy        345 ----------------------------AGAAATTTCACAAGCTATGGAACAAGAAGGT 375
                                           ||||||||||||||||||||||||||||||
Db        421 AAGTATGTTGGAATTCATTCTTCTTTTGCAGAAATTTCACAAGCTATGGAACAAGAAGGT 480

Qy        376 GCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGT 540

Qy        436 CACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCT 600

Qy        496 GCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTC 660

Qy        556 CGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGA 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGA 720

Qy        616 AGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTC 675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTC 780

Qy        676 TTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCC 735
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCC 840

Qy        736 AGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTG 795
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTG 900
```

```
Qy       796 TTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTC 855
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 TTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTC 960

Qy       856 TGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAG 915
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 TGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAG 1020

Qy       916 GTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTC 975
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTC 1080

Qy       976 AAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGA 1035
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 AAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGA 1140

Qy      1036 ATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCG 1095
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 ATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCG 1200

Qy      1096 ATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATC 1155
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 ATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATC 1260

Qy      1156 TGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACG 1215
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 TGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACG 1320

Qy      1216 CTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGG 1275
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 CTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGG 1380

Qy      1276 CGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAG 1335
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 CGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAG 1440

Qy      1336 GGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGG 1395
            |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db      1441 GGAGTGTGGAATAGGAAGTCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGG 1500

Qy      1396 GAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAG 1455
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 GAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAG 1560

Qy      1456 GAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTG 1515
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 GAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTG 1620

Qy      1516 TTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGG 1575
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 TTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGG 1680

Qy      1576 TCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTG 1635
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 TCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTG 1740

Qy      1636 TTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTT 1695
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 TTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTT 1800

Qy      1696 CCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAAT 1755
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 CCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAAT 1860

Qy      1756 GCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAA 1815
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 GCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAA 1920

Qy      1816 GAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAAC 1875
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 GAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAAC 1980

Qy      1876 CTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGG 1935
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 CTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGG 2040

Qy      1936 GTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCT 1995
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 GTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCT 2100

Qy      1996 CTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTT 2055
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 CTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTT 2160

Qy      2056 GGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCC 2115
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 GGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCC 2220

Qy      2116 ATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTT 2175
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 ATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTT 2280

Qy      2176 AGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGT 2235
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 AGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGT 2340

Qy      2236 AACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCG 2295
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 AACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCG 2400

Qy      2296 TGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGA 2355
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 TGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGA 2460

Qy      2356 TTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAA 2415
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 TTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAA 2520

Qy      2416 TCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCC 2475
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 TCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCC 2580

Qy      2476 TTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCC 2535
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 TTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCC 2640

Qy      2536 ACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGC 2595
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 ACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGC 2700

Qy      2596 CTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTT 2655
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 CTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTT 2760

Qy      2656 CCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGT 2715
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 CCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGT 2820

Qy      2716 GGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATG 2775
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 GGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATG 2880

Qy      2776 AACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGT 2835
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2881 AACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGT 2940

Qy      2836 CATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTG 2895
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941 CATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTG 3000

Qy      2896 TCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTG 2955
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001 TCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTG 3060

Qy      2956 GGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACG 3015
            |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
```

```
Db       3061 GGTGACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACG 3120

Qy       3016 AGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCC 3075
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 AGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCC 3180

Qy       3076 CTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAA 3135
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAA 3240

Qy       3136 GGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGG 3195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 GGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGG 3300

Qy       3196 CTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTC 3255
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 CTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTC 3360

Qy       3256 AAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db       3361 AAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGGTAC 3417


RESULT 7
US-10-416-642-3
; Sequence 3, Application US/10416642
; Publication No. US20040043452A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  ARVIZU, Chandra
;  TITLE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS
;  FILE REFERENCE: PF-0842 PCT
;  CURRENT APPLICATION NUMBER: US/10/416,642
;  CURRENT FILING DATE:  2003-05-13
;  PRIOR APPLICATION NUMBER: 60/249,407
;  PRIOR FILING DATE: 2000-11-15
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PERL Program
; SEQ ID NO 3
;   LENGTH: 3489
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040043452A1 7474830CB1
US-10-416-642-3

  Query Match             77.7%;  Score 3133.6;  DB 17;  Length 3489;
  Best Local Similarity   95.2%;  Pred. No. 0;
  Matches 3308;  Conservative    0;  Mismatches    4;  Indels  162;  Gaps    1;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAATTCACCAGAA 300

Qy        290 ---------------------------------------------------------- 289

Db        301 GATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGAAAATAAA 360

Qy        290 ---------------------------------------------------------- 289

Db        361 TATGGCATGACTAAGCTTATCTTGGGGGTGTCTGACATCTCTGACTCGAATAATAAACAC 420

Qy        290 ------------------------------AAATTTCACAAGCTATGGAACAAGAAGGT 318
                                           ||||||||||||||||||||||||||||||
Db        421 AAGTATGTTGGAATTCATTCTTCTTTTGCAGAAATTTCACAAGCTATGGAACAAGAAGGT 480

Qy        319 GCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCC 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCC 540

Qy        379 ACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGTCAC 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGTCAC 600

Qy        439 GTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCT 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCT 660

Qy        499 GACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGG 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGG 720

Qy        559 CCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGG 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGG 780

Qy        619 ATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTC 678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTC 840

Qy        679 CTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGG 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGG 900

Qy        739 GAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTG 798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTG 960

Qy        799 TTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGC 858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGC 1020

Qy        859 AAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTC 918
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTC 1080

Qy        919 CTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAG 978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAG 1140

Qy        979 TCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGGAACAAAGAATC 1038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGGAACAAAGAATC 1200

Qy       1039 CACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATC 1098
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATC 1260

Qy       1099 ATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGC 1158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGC 1320

Qy       1159 GTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTC 1218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTC 1380

Qy       1219 ACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGC 1278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1381 ACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGC 1440

Qy       1279 TGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGA 1338
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGA 1500

Qy       1339 GTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAG 1398
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1501 GTGTGGAATAGGAAGTCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAG 1560

Qy       1399 TCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAG 1458
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAG 1620

Qy       1459 TACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTA 1518
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTA 1680

Qy       1519 GAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCC 1578
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCC 1740

Qy       1579 ATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTT 1638
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 ATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTT 1800

Qy       1639 GGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCC 1698
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCC 1860

Qy       1699 CTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCC 1758
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCC 1920

Qy       1759 ACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAG 1818
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 ACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAG 1980

Qy       1819 TTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTG 1878
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTG 2040

Qy       1879 GACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTG 1938
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 GACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTG 2100

Qy       1939 GATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTA 1998
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTA 2160

Qy       1999 TGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGC 2058
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 TGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGC 2220

Qy       2059 ACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATG 2118
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 ACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATG 2280

Qy       2119 AAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGA 2178
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 AAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGA 2340

Qy       2179 AATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAAC 2238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 AATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAAC 2400

Qy       2239 CTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGT 2298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 CTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGT 2460

Qy       2299 GAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTG 2358
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTG 2520

Qy       2359 ACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCT 2418
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 ACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCT 2580

Qy       2419 CTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTG 2478
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 CTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTG 2640

Qy       2479 AGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACG 2538
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 AGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACG 2700

Qy       2539 GGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTA 2598
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTA 2760

Qy       2599 TCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCC 2658
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCC 2820

Qy       2659 CACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGT 2718
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGT 2880

Qy       2719 TTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAAC 2778
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 TTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAAC 2940

Qy       2779 CCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCAT 2838
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCAT 3000

Qy       2839 CTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCC 2898
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 CTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCC 3060

Qy       2899 TGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGT 2958
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGT 3120

Qy       2959 GACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGA 3018
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       3121 GACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGA 3180

Qy       3019 CTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTT 3078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTT 3240

Qy       3079 TCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGA 3138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGA 3300

Qy       3139 ATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTG 3198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 ATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTG 3360

Qy       3199 TGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAG 3258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 TGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAG 3420

Qy       3259 CCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312
             ||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db       3421 CCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGGTAC 3474
```

RESULT 8
US-10-216-645-1
; Sequence 1, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; APPLICANT: LESSL, MONIKA

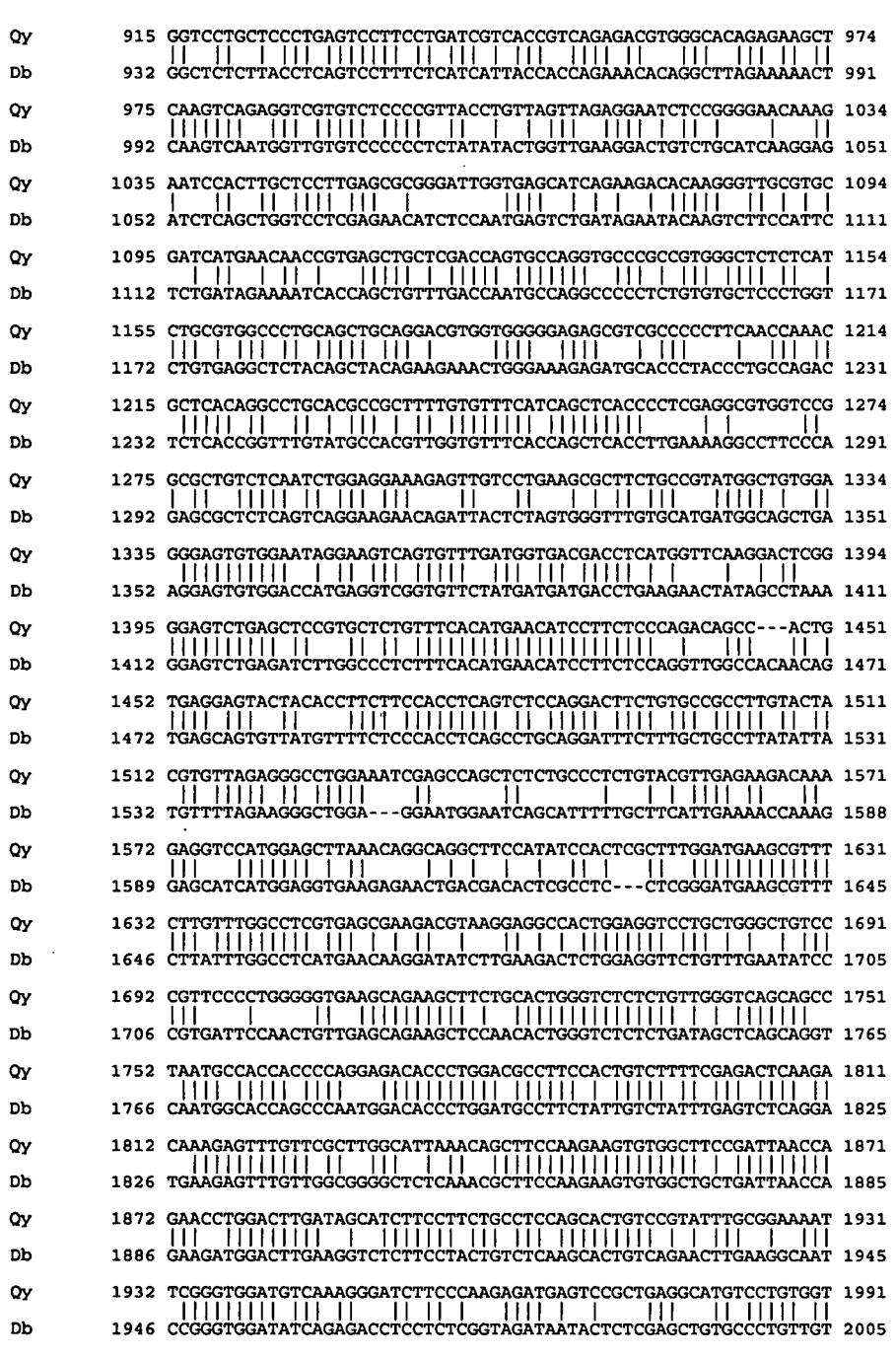
```
;  APPLICANT:  PETERS-KOTTIG, MICHAELE
;  APPLICANT:  BECKMANN, GEORG
;  TITLE OF INVENTION: HUMAN MATER PROTEINS
;  FILE REFERENCE: SCH-1910
;  CURRENT APPLICATION NUMBER: US/10/216,645
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 3926
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-216-645-1

  Query Match             77.7%;  Score 3133.6;  DB 15;  Length 3926;
  Best Local Similarity   95.2%;  Pred. No. 0;
  Matches 3308;  Conservative    0;  Mismatches    4;  Indels  162;  Gaps    1;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAATTCACCAGAA 300

Qy        290 ---------------------------------------------------------- 289

Db        301 GATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGAAAATAAA 360

Qy        290 ---------------------------------------------------------- 289

Db        361 TATGGCATGACTAAGCTTATCTTGGGGGTGTCTGACATCTCTGACTCGAATAATAAACAC 420

Qy        290 ------------------------------AAATTTCACAAGCTATGGAACAAGAAGGT 318
                                           ||||||||||||||||||||||||||||||
Db        421 AAGTATGTTGGAATTCATTCTTCTTTTGCAGAAATTTCACAAGCTATGGAACAAGAAGGT 480

Qy        319 GCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCC 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCC 540

Qy        379 ACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGTCAC 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGTCAC 600

Qy        439 GTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCT 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCT 660

Qy        499 GACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGG 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGG 720

Qy        559 CCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGG 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGG 780

Qy        619 ATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTC 678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTC 840

Qy        679 CTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGG 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGG 900

Qy        739 GAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTG 798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTG 960

Qy        799 TTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGC 858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGC 1020

Qy        859 AAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTC 918
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTC 1080

Qy        919 CTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAG 978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAG 1140

Qy        979 TCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATC 1038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATC 1200

Qy       1039 CACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATC 1098
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATC 1260

Qy       1099 ATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGC 1158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGC 1320

Qy       1159 GTGGCCCTGCAGCTGCAGGACGTGGTGGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTC 1218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTGGCCCTGCAGCTGCAGGACGTGGTGGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTC 1380

Qy       1219 ACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGC 1278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGC 1440

Qy       1279 TGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGA 1338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGA 1500

Qy       1339 GTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAG 1398
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1501 GTGTGGAATAGGAAGTCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAG 1560

Qy       1399 TCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAG 1458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAG 1620

Qy       1459 TACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTA 1518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTA 1680

Qy       1519 GAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCC 1578
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCC 1740

Qy       1579 ATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTT 1638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 ATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTT 1800

Qy       1639 GGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCC 1698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCC 1860

Qy       1699 CTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCC 1758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1861 CTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCC 1920

Qy       1759 ACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAG 1818
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 ACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAG 1980

Qy       1819 TTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTG 1878
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTG 2040

Qy       1879 GACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTG 1938
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 GACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTG 2100

Qy       1939 GATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTA 1998
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTA 2160

Qy       1999 TGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGC 2058
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 TGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGC 2220

Qy       2059 ACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATG 2118
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 ACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATG 2280

Qy       2119 AAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGA 2178
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 AAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGA 2340

Qy       2179 AATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAAC 2238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 AATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAAC 2400

Qy       2239 CTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGT 2298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 CTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGT 2460

Qy       2299 GAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTG 2358
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTG 2520

Qy       2359 ACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCT 2418
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 ACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCT 2580

Qy       2419 CTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTG 2478
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 CTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTG 2640

Qy       2479 AGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACG 2538
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 AGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACG 2700

Qy       2539 GGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTA 2598
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTA 2760

Qy       2599 TCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCC 2658
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCC 2820

Qy       2659 CACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGT 2718
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGT 2880

Qy       2719 TTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAAC 2778
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 TTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAAC 2940

Qy       2779 CCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCAT 2838
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCAT 3000

Qy       2839 CTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCC 2898
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 CTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCC 3060

Qy       2899 TGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGT 2958
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGT 3120

Qy       2959 GACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGA 3018
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGA 3180

Qy       3019 CTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTT 3078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTT 3240

Qy       3079 TCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGA 3138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGA 3300

Qy       3139 ATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTG 3198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 ATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTG 3360

Qy       3199 TGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAG 3258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 TGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAG 3420

Qy       3259 CCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||
Db       3421 CCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGGTAC 3474
```

RESULT 9
US-10-092-900A-347
; Sequence 347, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev,, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A

```
;  CURRENT FILING DATE:  2002-03-07
;  PRIOR APPLICATION NUMBER: USSN 60/274,322
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/283,675
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: USSN 60/338,092
;  PRIOR FILING DATE: 2001-12-03
;  PRIOR APPLICATION NUMBER: USSN 60/274,281
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/274,191
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/325,681
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: USSN 60/304,354
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: USSN 60/279,995
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: USSN 60/294,899
;  PRIOR FILING DATE: 2001-05-31
;  PRIOR APPLICATION NUMBER: USSN 60/287,424
;  PRIOR FILING DATE: 2001-04-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 347
;   LENGTH: 3226
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (69)..(3168)
US-10-092-900A-347

  Query Match            71.9%;  Score 2900.6;  DB 17;  Length 3226;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 2903;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        406 CATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAG 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 CATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAG 308

Qy        466 GATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCT 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCT 368

Qy        526 GGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAG 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAG 428

Qy        586 TCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGA 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGA 488

Qy        646 CTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAG 705
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAG 548

Qy        706 AAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTG 765
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 AAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTG 608

Qy        766 ACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTG 825
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 ACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTG 668

Qy        826 GGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCG 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCG 728

Qy        886 TTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTC 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTC 788

Qy        946 ACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTG 1005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 ACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTG 848

Qy       1006 TTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGT 1065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 TTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGT 908

Qy       1066 GAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAG 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 GAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAG 968

Qy       1126 TGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTG 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 TGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTG 1028

Qy       1186 GGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTT 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1029 GGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTT 1088

Qy       1246 CATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTC 1305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 CATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTC 1148

Qy       1306 CTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGAT 1365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1149 CTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGAC 1208

Qy       1366 GGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATG 1425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1209 GGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATG 1268

Qy       1426 AACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTC 1485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1269 AACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTC 1328

Qy       1486 CAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTC 1545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1329 CAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTC 1388

Qy       1546 TGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCAT 1605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1389 TGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCAT 1448

Qy       1606 ATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGG 1665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1449 ATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGG 1508

Qy       1666 CCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCAC 1725
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1509 CCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCAC 1568

Qy       1726 TGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCC 1785
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1569 TGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCC 1628

Qy       1786 TTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTC 1845
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1629 TTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTC 1688

Qy       1846 CAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTC 1905
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1689 CAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTC 1748

Qy       1906 CAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGAT 1965
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1749 CAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGAT 1808

Qy       1966 GAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAG 2025
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 GAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAG 1868

Qy       2026 GAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGAC 2085
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1869 GAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGAC 1928

Qy       2086 CTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCAT 2145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1929 CTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCAT 1988

Qy       2146 CCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAG 2205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1989 CCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAG 2048

Qy       2206 CACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACC 2265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2049 CACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACC 2108

Qy       2266 CACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTG 2325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2109 CACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTG 2168

Qy       2326 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2169 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2228

Qy       2386 CAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACA 2445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2229 CAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACA 2288

Qy       2446 GACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAG 2505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2289 GACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAG 2348

Qy       2506 CTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTC 2565
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2349 CTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTC 2408

Qy       2566 GTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGT 2625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2409 GTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGT 2468

Qy       2626 GTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTG 2685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2469 GTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTG 2528

Qy       2686 AATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAAC 2745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2529 AATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAAC 2588

Qy       2746 TCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTT 2805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2589 TCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTT 2648

Qy       2806 CTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGT 2865
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2649 CTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGT 2708

Qy       2866 CATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTG 2925
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2709 CATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTG 2768

Qy       2926 AAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAG 2985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2769 AAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAG 2828

Qy       2986 GGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACT 3045
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2829 GGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACT 2888

Qy       3046 TCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTA 3105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2889 TCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTA 2948

Qy       3106 AACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCC 3165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2949 AACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCC 3008

Qy       3166 TGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATA 3225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3009 TGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATA 3068

Qy       3226 AGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGG 3285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3069 AGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGG 3128

Qy       3286 CATTCTTTTGATGAAGATGACCGACAC 3312
              |||||||||||||||||||||||| ||
Db       3129 CATTCTTTTGATGAAGATGACCGGTAC 3155


RESULT 10
US-10-399-443-5
; Sequence 5, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as Represented by the
;  APPLICANT:  Secretary, Department of Health & Human Services, The National Institute
;  APPLICANT:  Health
;  APPLICANT:  Nelson, Lawrence M.
;  APPLICANT:  Tong, Zhi-Bin
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Zhi-Bin, Tong
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64785
;  CURRENT APPLICATION NUMBER: US/10/399,443
;  CURRENT FILING DATE:  2003-04-16
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 3447
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-399-443-5

  Query Match            31.7%;  Score 1278;  DB 17;  Length 3447;
  Best Local Similarity  67.2%;  Pred. No. 0;
  Matches 1898;  Conservative    0;  Mismatches  908;  Indels   18;  Gaps    6;

Qy        498 TGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCG 557
              |||| | || || ||| ||   ||| ||| |||||||| |  || ||| |     |||||
Db        515 TGACAGCCCAGAGATGAAATTATTGTCTGATGCTTTTAAACCATACCAGAAAACCTTCCA 574

Qy        558 GCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAG 617
              ||||| |||  |  | || || ||||   ||||| ||||||| || ||| | ||||||||
Db        575 GCCTCACACCATTATCCTACATGGAAGACCAGGAGTTGGGAAGTCAGCTTTGGCCAGAAG 634

Qy        618 GATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTT 677
              || || ||  ||||||| || |||  ||||| |||   ||||   ||||  ||| ||||
Db        635 TATTGTTCTTGGCTGGGCACAGGGTAAACTCTTCCAAAAAATG---TCCTTTGTCATCTT 691

Qy        678 CCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAG 737
              | || | |||||||| ||  || |||   || |||||||  |  || || | ||  | |
Db        692 CTTCTCTGTTAGAGAAATAAAGTGGACAGAGAAGAGCAGTTTGGCACAGCTGATTGCTAA 751

Qy        738 GGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTT 797
              |||||| |||||||||  || ||  |||||  |||||||||||| |||||||| || ||
Db        752 GGAGTGTCCAGACTCCTGGGATCTAGTGACAAAGATCATGTCCCAACCAGAAAGACTCTT 811

Qy        798 GTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC---AACAATGACACAAAGCT 854
              |||   |||| || || || |||||  ||| ||||||||||    |  |||| | |  ||
Db        812 GTTTGTCATAGATGGCTTGGATGATATGGACTCTGTCCTCCAACATGATGATATGACACT 871

Qy        855 CTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAA 914
              | || |||||||   ||  | |||||    | || ||| ||   ||| || |||||||||
Db        872 ATCCAGAGACTGGAAGGATGAACAGCCCATATACATCCTGATGTACAGCCTCCTGAGGAA 931
```


Qy 915 GGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCT 974
Db 932 GGCTCTCTTACCTCAGTCCTTTCTCATCATTACCACCAGAAACACAGGCTTAGAAAAACT 991
Qy 975 CAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAG 1034
Db 992 CAAGTCAATGGTTGTGTCCCCCCTCTATATACTGGTTGAAGGACTGTCTGCATCAAGGAG 1051
Qy 1035 AATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGC 1094
Db 1052 ATCTCAGCTGGTCCTCGAGAACATCTCCAATGAGTCTGATAGAATACAAGTCTTCCATTC 1111
Qy 1095 GATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCAT 1154
Db 1112 TCTGATAGAAAATCACCAGCTGTTTGACCAATGCCAGGCCCCCTCTGTGTGCTCCCTGGT 1171
Qy 1155 CTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAAC 1214
Db 1172 CTGTGAGGCTCTACAGCTACAGAAGAAACTGGGAAAGAGATGCACCCTACCCTGCCAGAC 1231
Qy 1215 GCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCG 1274
Db 1232 TCTCACCGGTTTGTATGCCACGTTGGTGTTTCACCAGCTCACCTTGAAAAGGCCTTCCCA 1291
Qy 1275 GCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGA 1334
Db 1292 GAGCGCTCTCAGTCAGGAAGAACAGATTACTCTAGTGGGTTTGTGCATGATGGCAGCTGA 1351
Qy 1335 GGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGG 1394
Db 1352 AGGAGTGTGGACCATGAGGTCGGTGTTCTATGATGATGACCTGAAGAACTATAGCCTAAA 1411
Qy 1395 GGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCC---ACTG 1451
Db 1412 GGAGTCTGAGATCTTGGCCCTCTTTCACATGAACATCCTTCTCCAGGTTGGCCACAACAG 1471
Qy 1452 TGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTA 1511
Db 1472 TGAGCAGTGTTATGTTTTCTCCCACCTCAGCCTGCAGGATTTCTTTGCTGCCTTATATTA 1531
Qy 1512 CGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAA 1571
Db 1532 TGTTTTAGAAGGGCTGGA---GGAATGGAATCAGCATTTTTGCTTCATTGAAAACCAAAG 1588
Qy 1572 GAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTT 1631
Db 1589 GAGCATCATGGAGGTGAAGAGAACTGACGACACTCGCCTC---CTCGGGATGAAGCGTTT 1645
Qy 1632 CTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCC 1691
Db 1646 CTTATTTGGCCTCATGAACAAGGATATCTTGAAGACTCTGGAGGTTCTGTTTGAATATCC 1705
Qy 1692 CGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCC 1751
Db 1706 CGTGATTCCAACTGTTGAGCAGAAGCTCCAACACTGGGTCTCTCTGATAGCTCAGCAGGT 1765
Qy 1752 TAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGA 1811
Db 1766 CAATGGCACCAGCCCAATGGACACCCTGGATGCCTTCTATTGTCTATTTGAGTCTCAGGA 1825
Qy 1812 CAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCA 1871
Db 1826 TGAAGAGTTTGTTGGCGGGGCTCTCAAACGCTTCCAAGAAGTGTGGCTGCTGATTAACCA 1885
Qy 1872 GAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAAT 1931
Db 1886 GAAGATGGACTTGAAGGTCTCTTCCTACTGTCTCAAGCACTGTCAGAACTTGAAGGCAAT 1945
Qy 1932 TCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGT 1991
Db 1946 CCGGGTGGATATCAGAGACCTCCTCTCGGTAGATAATACTCTCGAGCTGTGCCCTGTTGT 2005
Qy 1992 CCCTCTATGGATGCGGGA---TAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTC 2048
Db 2006 TACTGTCCAGGAGACACAATGTAAGCCCCTCCTCATGGAGTGGTGGGGAAACTTCTGCTC 2065
Qy 2049 CATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGA 2108
Db 2066 TGTGCTTGGCAGCCTCCGGAACTTGAAGGAGCTGGACTTGGGCGACAGCATCCTGAGTCA 2125
Qy 2109 GCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCT 2168
Db 2126 ACGGGCCATGAAGATACTGTGCCTCGAGCTGCGGAATCAGTCCTGCAGAATACAGAAGCT 2185
Qy 2169 GATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGC 2228
Db 2186 GACGTTTAAGAGTGCAGAGGTAGTGTCTGGCCTGAAACATCTCTGGAAGCTCCTTTTTAG 2245
Qy 2229 CAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAG 2288
Db 2246 CAATCAAAACTTAAAGTACCTCAATCTAGGGAACACTCCCATGAAGGATGATGACATGAA 2305
Qy 2289 GATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTG 2348
Db 2306 GTTAGCCTGCGAAGCGCTGAAACATCCAAAGTGCTCCGTGGAGACTCTGAGGTTGGATTC 2365
Qy 2349 CTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAG 2408
Db 2366 CTGTGAGTTAACCATCATTGGTTATGAGATGATCTCCACGCTTCTTATTTCAACCACCAG 2425
Qy 2409 CCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAG 2468
Db 2426 GCTAAAGTGTCTCAGCCTGGCCAAAAATAGAGTGGGAGTAAAAAGCATGATATCCCTTGG 2485
Qy 2469 TGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCAT 2528
Db 2486 GAATGCCTTGAGTAGCTCAATGTGTCTACTGCAAAAGTTGATACTGGACAACTGTGGCCT 2545
Qy 2529 CACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACA 2588
Db 2546 CACACCTGCCAGCTGCCACCTTCTGGTCTCAGCCCTTTTCAGCAACCAGAACTTGACACA 2605
Qy 2589 CCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCAT 2648
Db 2606 CCTGTGCCTGTCAAACAACAGCCTGGGGACTGAAGGAGTGCAACAGCTGTGTCAGTTCCT 2665
Qy 2649 GAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGC 2708
Db 2666 GAGGAATCCAGAATGTGCTCTCCAGCGGCTGATACTGAATCACTGCAACATTGTAGATGA 2725
Qy 2709 TGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCT 2768
Db 2726 TGCTTATGGCTTCCTGGCAATGAGACTTGCAAACAACACAAAGCTGACCCACCTGAGCCT 2785
Qy 2769 TAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACC 2828
Db 2786 GACCATGAACCCCGTAGGGGATGGTGCAATGAAGCTACTGTGTGAAGCTTTAAAGGAACC 2845
Qy 2829 ATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGA 2888
Db 2846 TACTTGTTACCTTCAAGAACTGGAACTAGTGGACTGCCAACTCACACAGAACTGCTGCGA 2905
Qy 2889 GAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAA 2948
Db 2906 GGACCTGGCCTGTATGATCACAACAACCAAGCACTTAAAAAGTTTGGATCTTGGTAACAA 2965
Qy 2949 TGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGT 3008
Db 2966 CGCCCTGGGTGACAAAGGAGTCATAACCCTGTGTGAGGGACTGAAGCAAAGTAGCAGCTC 3025
Qy 3009 TCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTC 3068
Db 3026 CCTGAGGAGACTTGGGTTGGGGGCATGTAAGTTGACTTCCAATTGCTGTGAGGCATTGTC 3085
Qy 3069 CTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAG 3128

```
Db       3086 ATTGGCCATCTCTTGCAACCCTCACCTGAACAGCCTAAACCTGGTGAAGAATGACTTCAG 3145

Qy       3129 TCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGAT 3188

Db       3146 TACATCGGGGATGTTGAAGCTGTGCTCTGCGTTCCAATGCCCTGTCTCTAACCTGGGGAT 3205

Qy       3189 AATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCA 3248

Db       3206 AATTGGCCTGTGGAAGCAGGAGTACTATGCCCGAGTGAGAAGACAGCTGGAGGAAGTTGA 3265

Qy       3249 GCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCG 3308

Db       3266 GTTTGTCAAGCCCCACGTGGTGATTGATGGTGATTGGTATGCTAGTGATGAAGATGACCG 3325

Qy       3309 ACAC 3312

Db       3326 AAAC 3329


RESULT 11
US-10-677-943-5
; Sequence 5, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 3447
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-677-943-5

  Query Match             31.7%;  Score 1278;  DB 17;  Length 3447;
  Best Local Similarity   67.2%;  Pred. No. 0;
  Matches 1898;  Conservative    0;  Mismatches  908;  Indels   18;  Gaps    6;

Qy        498 TGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCG 557

Db        515 TGACAGCCCAGAGATGAAATTATTGTCTGATGCTTTTAAACCATACCAGAAAACCTTCCA 574

Qy        558 GCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAG 617

Db        575 GCCTCACACCATTATCCTACATGGAAGACCAGGAGTTGGGAAGTCAGCTTTGGCCAGAAG 634

Qy        618 GATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTT 677

Db        635 TATTGTTCTTGGCTGGGCACAGGGTAAACTCTTCCAAAAAATG---TCCTTTGTCATCTT 691

Qy        678 CCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAG 737

Db        692 CTTCTCTGTTAGAGAAATAAAGTGGACAGAGAAGAGCAGTTTGGCACAGCTGATTGCTAA 751

Qy        738 GGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTT 797

Db        752 GGAGTGTCCAGACTCCTGGGATCTAGTGACAAAGATCATGTCCCAACCAGAAAGACTCTT 811

Qy        798 GTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC---AACAATGACACAAAGCT 854

Db        812 GTTTGTCATAGATGGCTTGGATGATATGGACTCTGTCCTCCAACATGATGATATGACACT 871

Qy        855 CTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAA 914

Db        872 ATCCAGAGACTGGAAGGATGAACAGCCCATATACATCCTGATGTACAGCCTCCTGAGGAA 931

Qy        915 GGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCT 974

Db        932 GGCTCTCTTACCTCAGTCCTTTCTCATCATTACCACCAGAAACACAGGCTTAGAAAAACT 991

Qy        975 CAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAG 1034

Db        992 CAAGTCAATGGTTGTGTCCCCCCTCTATATACTGGTTGAAGGACTGTCTGCATCAAGGAG 1051

Qy       1035 AATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGC 1094

Db       1052 ATCTCAGCTGGTCCTCGAGAACATCTCCAATGAGTCTGATAGAATACAAGTCTTCCATTC 1111

Qy       1095 GATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCAT 1154

Db       1112 TCTGATAGAAAATCACCAGCTGTTTGACCAATGCCAGGCCCCCTCTGTGTGCTCCCTGGT 1171

Qy       1155 CTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAAC 1214

Db       1172 CTGTGAGGCTCTACAGCTACAGAAGAAACTGGGAAAGAGATGCACCCTACCCTGCCAGAC 1231

Qy       1215 GCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCG 1274

Db       1232 TCTCACCGGTTTGTATGCCACGTTGGTGTTTCACCAGCTCACCTTGAAAAGGCCTTCCCA 1291

Qy       1275 GCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGA 1334

Db       1292 GAGCGCTCTCAGTCAGGAAGAACAGATTACTCTAGTGGGTTTGTGCATGATGGCAGCTGA 1351

Qy       1335 GGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGG 1394

Db       1352 AGGAGTGTGGACCATGAGGTCGGTGTTCTATGATGATGACCTGAAGAACTATAGCCTAAA 1411

Qy       1395 GGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCC---ACTG 1451

Db       1412 GGAGTCTGAGATCTTGGCCCTCTTTCACATGAACATCCTTCTCCAGGTTGGCCACAACAG 1471

Qy       1452 TGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTA 1511

Db       1472 TGAGCAGTGTTATGTTTTCTCCCACCTCAGCCTGCAGGATTTCTTTGCTGCCTTATATTA 1531

Qy       1512 CGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAA 1571

Db       1532 TGTTTTAGAAGGGCTGGA---GGAATGGAATCAGCATTTTTGCTTCATTGAAAACCAAAG 1588

Qy       1572 GAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTT 1631

Db       1589 GAGCATCATGGAGGTGAAGAGAACTGACGACACTCGCCTC---CTCGGGATGAAGCGTTT 1645

Qy       1632 CTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCC 1691

Db       1646 CTTATTTGGCCTCATGAACAAGGATATCTTGAAGACTCTGGAGGTTCTGTTTGAATATCC 1705

Qy       1692 CGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCC 1751

Db       1706 CGTGATTCCAACTGTTGAGCAGAAGCTCCAACACTGGGTCTCTCTGATAGCTCAGCAGGT 1765

Qy       1752 TAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGA 1811

Db       1766 CAATGGCACCAGCCCAATGGACACCCTGGATGCCTTCTATTGTCTATTTGAGTCTCAGGA 1825

Qy       1812 CAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCA 1871

Db       1826 TGAAGAGTTTGTTGGCGGGGCTCTCAAACGCTTCCAAGAAGTGTGGCTGCTGATTAACCA 1885

Qy       1872 GAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAAT 1931
```

```
Db       1886 GAAGATGGACTTGAAGGTCTCTTCCTACTGTCTCAAGCACTGTCAGAACTTGAAGGCAAT 1945

Qy       1932 TCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGT 1991
              ||||||||| ||| ||   || || |  |||| |  |    |||  || ||||| ||
Db       1946 CCGGGTGGATATCAGAGACCTCCTCTCGGTAGATAATACTCTCGAGCTGTGCCCTGTTGT 2005

Qy       1992 CCCTCTATGGATGCGGGA---TAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTC 2048
              ||  |   |   |    |  |||| ||||| |   ||||  |||||  | | ||||||||
Db       2006 TACTGTCCAGGAGACACAATGTAAGCCCCTCCTCATGGAGTGGTGGGGAAACTTCTGCTC 2065

Qy       2049 CATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGA 2108
              |||||||||  ||  ||   || ||  | ||||||||  |||||  ||||||||||    |
Db       2066 TGTGCTTGGCAGCCTCCGGAACTTGAAGGAGCTGGACTTGGGCGACAGCATCCTGAGTCA 2125

Qy       2109 GCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCT 2168
              ||||||||||||  |||||   | |||||  || |||   ||||||  |||||||  ||
Db       2126 ACGGGCCATGAAGATACTGTGCCTCGAGCTGCGGAATCAGTCCTGCAGAATACAGAAGCT 2185

Qy       2169 GATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGC 2228
              ||  |||||   | ||||  || |     ||||  || | ||  |||||||    ||  |   |
Db       2186 GACGTTTAAGAGTGCAGAGGTAGTGTCTGGCCTGAAACATCTCTGGAAGCTCCTTTTTAG 2245

Qy       2229 CAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAG 2288
              |||  |  |||  |||  | ||||||  | ||   |||  | |  |||||||  ||  ||   | |
Db       2246 CAATCAAAACTTAAAGTACCTCAATCTAGGGAACACTCCCATGAAGGATGATGACATGAA 2305

Qy       2289 GATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTG 2348
              | | || ||  |||||  | |||||  |||||  || |   |||||  ||  |||||  ||||||
Db       2306 GTTAGCCTGCGAAGCGCTGAAACATCCAAAGTGCTCCGTGGAGACTCTGAGGTTGGATTC 2365

Qy       2349 CTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAG 2408
              |||||  ||  |||          ||||   ||  ||||||||     |  ||||    ||  ||||
Db       2366 CTGTGAGTTAACCATCATTGGTTATGAGATGATCTCCACGCTTCTTATTTCAACCACCAG 2425

Qy       2409 CCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAG 2468
              ||  ||  |  ||| ||||||||    |||  |   |||   ||    |   |  ||  |  ||  |
Db       2426 GCTAAAGTGTCTCAGCCTGGCCAAAAATAGAGTGGGAGTAAAAAGCATGATATCCCTTGG 2485

Qy       2469 TGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCAT 2528
              ||||||||||    |||    |||    |||||  ||| ||||||||||  ||||||||  |
Db       2486 GAATGCCTTGAGTAGCTCAATGTGTCTACTGCAAAAGTTGATACTGGACAACTGTGGCCT 2545

Qy       2529 CACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACA 2588
              ||||  |   |  ||||||     |||||  |||||||||   |||||||||  ||  |||||||||
Db       2546 CACACCTGCCAGCTGCCACCTTCTGGTCTCAGCCCTTTTCAGCAACCAGAACTTGACACA 2605

Qy       2589 CCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCAT 2648
              |||||||| || ||||||||||||||||  |||||  ||  |  |  |||||||  |  |  |
Db       2606 CCTGTGCCTGTCAAACAACAGCCTGGGGACTGAAGGAGTGCAACAGCTGTGTCAGTTCCT 2665

Qy       2649 GAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGC 2708
              ||||   |||   | |||   ||| ||| |||||||  ||||||||  |||  ||  |  |
Db       2666 GAGGAATCCAGAATGTGCTCTCCAGCGGCTGATACTGAATCACTGCAACATTGTAGATGA 2725

Qy       2709 TGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCT 2768
              ||   | |||  ||  ||| |     |||       ||| ||  ||||||  ||||||||||
Db       2726 TGCTTATGGCTTCCTGGCAATGAGACTTGCAAACAACACAAAGCTGACCCACCTGAGCCT 2785

Qy       2769 TAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACC 2828
              |  |||||||||  ||  |   ||   |||||||  |||||  ||  |   |  |  |||||
Db       2786 GACCATGAACCCCGTAGGGGATGGTGCAATGAAGCTACTGTGTGAAGCTTTAAAGGAACC 2845

Qy       2829 ATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGA 2888
              |||||  |  ||  ||  ||  |||||   |  ||   |  ||  ||  |||||        |||||  ||
Db       2846 TACTTGTTACCTTCAAGAACTGGAACTAGTGGACTGCCAACTCACACAGAACTGCTGCGA 2905

Qy       2889 GAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAA 2948
              |   |||  |||||  |||||  |  |   |  ||   |||  |  ||  ||   |||||||      ||||
Db       2906 GGACCTGGCCTGTATGATCACAACAACCAAGCACTTAAAAAGTTTGGATCTTGGTAACAA 2965

Qy       2949 TGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGT 3008
              ||||||||||||   ||  ||    |  |||||  ||||||||||||||||   |  |||
Db       2966 CGCCCTGGGTGACAAAGGAGTCATAACCCTGTGTGAGGGACTGAAGCAAAGTAGCAGCTC 3025

Qy       3009 TCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTC 3068
              |||| ||||||  ||||||  |||||||     |||||||  |||||||||||||| | ||
Db       3026 CCTGAGGAGACTTGGGTTGGGGGCATGTAAGTTGACTTCCAATTGCTGTGAGGCATTGTC 3085

Qy       3069 CTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAG 3128
              ||||||  | ||  |||||||   || ||||  |||  ||||||||||||  |||||  |||||||
Db       3086 ATTGGCCATCTCTTGCAACCCTCACCTGAACAGCCTAAACCTGGTGAAGAATGACTTCAG 3145

Qy       3129 TCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGAT 3188
              | |    ||  |||  ||||||||||  ||  ||  ||    ||  ||    ||||||  |   |||
Db       3146 TACATCGGGGATGTTGAAGCTGTGCTCTGCGTTCCAATGCCCTGTCTCTAACCTGGGGAT 3205

Qy       3189 AATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCA 3248
              ||||||  ||||||||    | |||||  ||  |  |  ||  |  |  ||||||||||||  |
Db       3206 AATTGGCCTGTGGAAGCAGGAGTACTATGCCCGAGTGAGAAGACAGCTGGAGGAAGTTGA 3265

Qy       3249 GCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCG 3308
              | |  |||||||||  ||  ||  |||||  |||  ||||  ||  ||  ||||||||||||||
Db       3266 GTTTGTCAAGCCCCACGTGGTGATTGATGGTGATTGGTATGCTAGTGATGAAGATGACCG 3325

Qy       3309 ACAC 3312
              |  ||
Db       3326 AAAC 3329
```

RESULT 12
US-10-399-443-1
; Sequence 1, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-399-443-1

Query Match 28.6%; Score 1152.8; DB 17; Length 1157;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        754 CAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGT 813
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAAGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGT 60

Qy        814 TTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAG 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAG 120

Qy        874 AAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCC 180

Qy        934 TTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCT 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCT 240
```

```
Qy        994 CCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAG 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAG 300

Qy       1054 CGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAG 360

Qy       1114 CTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTG 420

Qy       1174 CAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCC 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCC 480

Qy       1234 GCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAG 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAG 540

Qy       1294 GAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAG 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAG 600

Qy       1354 TCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCT 1413
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCT 660

Qy       1414 CTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTC 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTC 720

Qy       1474 CACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATC 1533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATC 780

Qy       1534 GAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAG 1593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAG 840

Qy       1594 GCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAA 1653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAA 900

Qy       1654 GACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAG 1713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAG 960

Qy       1714 AAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGAC 1773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGAC 1020

Qy       1774 ACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCA 1833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCA 1080

Qy       1834 TTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCT 1893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCT 1140

Qy       1894 TCCTTCTGCCTCCAGC 1909
              ||||||||||||||||
Db       1141 TCCTTCTGCCTCCAGC 1156


RESULT 13
US-10-677-943-1
; Sequence 1, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 1157
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-677-943-1

  Query Match            28.6%;  Score 1152.8;  DB 17;  Length 1157;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1154;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        754 CAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGT 813
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAAGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGT 60

Qy        814 TTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAG 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAG 120

Qy        874 AAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCC 180

Qy        934 TTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCT 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCT 240

Qy        994 CCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAG 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAG 300

Qy       1054 CGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAG 360

Qy       1114 CTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTG 420

Qy       1174 CAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCC 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCC 480

Qy       1234 GCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAG 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAG 540

Qy       1294 GAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAG 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAG 600

Qy       1354 TCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCT 1413
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCT 660

Qy       1414 CTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTC 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTC 720
```

```
Qy       1474 CACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATC 1533
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATC 780

Qy       1534 GAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAG 1593
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 GAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAG 840

Qy       1594 GCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAA 1653
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 GCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAA 900

Qy       1654 GACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAG 1713
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAG 960

Qy       1714 AAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGAC 1773
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGAC 1020

Qy       1774 ACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCA 1833
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 ACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCA 1080

Qy       1834 TTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCT 1893
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 TTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCT 1140

Qy       1894 TCCTTCTGCCTCCAGC 1909
             ||||||||||||||||
Db        1141 TCCTTCTGCCTCCAGC 1156
```

RESULT 14
US-10-399-443-3
; Sequence 3, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1075
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-399-443-3

Query Match 18.8%; Score 756.6; DB 17; Length 1075;
Best Local Similarity 99.5%; Pred. No. 1.3e-215;
Matches 759; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2550 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 2609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 60

Qy       2610 CCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCT 2669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCT 120

Qy       2670 GCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACT 2729
             ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db         121 GCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTCTCTTGCACT 180

Qy       2730 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 2789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 240

Qy       2790 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 2849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 300

Qy       2850 GGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 2909
             ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GGAGTTGGTAAAATGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 360

Qy       2910 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 2969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 420

Qy       2970 TGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 3029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 480

Qy       3030 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 3089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 540

Qy       3090 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 3149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 600

Qy       3150 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 3209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 660

Qy       3210 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 3269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 720

Qy       3270 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312
             |||||||||||||||||||||||||||||||||||||||||||  ||
Db         721 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGGTAC 763
```

RESULT 15
US-10-677-943-3
; Sequence 3, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677,943
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1075
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-677-943-3

```
  Query Match            18.8%;  Score 756.6;  DB 17;  Length 1075;
  Best Local Similarity  99.5%;  Pred. No. 1.3e-215;
  Matches  759;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2550 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 2609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 60

Qy       2610 CCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCT 2669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCT 120

Qy       2670 GCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACT 2729
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        121 GCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTCTCTTGCACT 180

Qy       2730 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 2789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 240

Qy       2790 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 2849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 300

Qy       2850 GGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 2909
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAGTTGGTAAAATGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 360

Qy       2910 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 2969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 420

Qy       2970 TGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 3029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 480

Qy       3030 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 3089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 540

Qy       3090 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 3149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 600

Qy       3150 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 3209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 660

Qy       3210 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 3269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 720

Qy       3270 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312
             |||||||||||||||||||||||||||||||||||||  ||
Db        721 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGGTAC 763


Search completed: February  4, 2005, 18:01:03
Job time : 2045 secs
```

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 4, 2005, 21:16:28 ; Search time 1552 Seconds
(without alignments)
4984.354 Million cell updates/sec

Title: US-10-066-521-6
Perfect score: 1344
Sequence: 1 MEGDKSLTFSSYGLQWCLYE.....DDHSGVSWSLGAAGLEGLVS 1344

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4313806 seqs, 2877871033 residues

Word size: 1

Total number of hits satisfying chosen parameters: 8617573

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10066521/runat_04022005_114650_4827/app_query.fasta_1.1543
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=oli.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10066521_@CGN_1_1_876_@runat_04022005_114650_4827
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1344	100.0	4035	14	US-10-124-498-5	Sequence 5, Appli
2		1344	100.0	4035	14	US-10-066-521-5	Sequence 5, Appli
3		1006	74.9	3489	17	US-10-416-642-3	Sequence 3, Appli
4		1006	74.9	3926	15	US-10-216-645-1	Sequence 1, Appli
5		988	73.5	3830	15	US-10-216-645-3	Sequence 3, Appli
6		968	72.0	3226	17	US-10-092-900A-347	Sequence 347, App
7		616	45.8	3885	18	US-10-860-761-3	Sequence 3, Appli
8		616	45.8	3900	17	US-10-399-443-23	Sequence 23, Appl
9		616	45.8	3900	17	US-10-677-943-23	Sequence 23, Appl
10		385	28.6	1157	17	US-10-399-443-1	Sequence 1, Appli
11		385	28.6	1157	17	US-10-677-943-1	Sequence 1, Appli
12		196	14.6	1075	17	US-10-399-443-3	Sequence 3, Appli
13		196	14.6	1075	17	US-10-677-943-3	Sequence 3, Appli
14		57	4.2	2099	13	US-10-027-632-258159	Sequence 258159,
15		57	4.2	2099	17	US-10-027-632-258159	Sequence 258159,
16	c	12	0.9	509	16	US-10-029-386-10957	Sequence 10957, A
17	c	12	0.9	1704	16	US-10-029-386-24660	Sequence 24660, A
18		12	0.9	3108	10	US-09-965-621-23	Sequence 23, Appl
19		12	0.9	3108	17	US-10-407-866-23	Sequence 23, Appl
20		12	0.9	3108	18	US-10-781-294-23	Sequence 23, Appl
21		12	0.9	3186	14	US-10-124-498-17	Sequence 17, Appl
22		12	0.9	3186	14	US-10-066-521-17	Sequence 17, Appl
23		12	0.9	3218	17	US-10-407-866-67	Sequence 67, Appl
24		12	0.9	3447	17	US-10-399-443-5	Sequence 5, Appli
25		12	0.9	3447	17	US-10-677-943-5	Sequence 5, Appli
26		12	0.9	3466	17	US-10-108-260A-718	Sequence 718, App
27		12	0.9	4931	15	US-10-028-374-1	Sequence 1, Appli
28		12	0.9	4931	16	US-10-183-770-1	Sequence 1, Appli
29	c	10	0.7	610	17	US-10-424-599-139217	Sequence 139217,
30	c	9	0.7	240	16	US-10-029-386-16506	Sequence 16506, A
31		9	0.7	270	11	US-09-922-293-1943	Sequence 1943, Ap
32	c	9	0.7	339	18	US-10-437-963-46914	Sequence 46914, A
33	c	9	0.7	346	18	US-10-425-115-150063	Sequence 150063,
34		9	0.7	394	18	US-10-425-115-72548	Sequence 72548, A
35	c	9	0.7	426	18	US-10-674-124A-25173	Sequence 25173, A
36	c	9	0.7	438	18	US-10-357-930-38072	Sequence 38072, A
37		9	0.7	440	17	US-10-424-599-35497	Sequence 35497, A
38	c	9	0.7	564	16	US-10-029-386-2806	Sequence 2806, Ap
39		9	0.7	578	10	US-09-764-891-1745	Sequence 1745, Ap
40		9	0.7	693	18	US-10-363-345A-27001	Sequence 27001, A
41	c	9	0.7	693	18	US-10-363-345A-27002	Sequence 27002, A
42		9	0.7	693	18	US-10-363-345A-27115	Sequence 27115, A
43	c	9	0.7	693	18	US-10-363-345A-27116	Sequence 27116, A
44		9	0.7	720	13	US-10-027-632-150437	Sequence 150437,
45		9	0.7	720	17	US-10-027-632-150437	Sequence 150437,

ALIGNMENTS

RESULT 1
US-10-124-498-5
; Sequence 5, Application US/10124498
; Publication No. US20030017983A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-367001
; CURRENT APPLICATION NUMBER: US/10/124,498
; CURRENT FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 10/066,521
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 4035
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(4032)
US-10-124-498-5

Alignment Scores:
Pred. No.:              0           Length:        4035
Score:                  1344.00     Matches:       1344
Percent Similarity:     100.00%     Conservative:  0
Best Local Similarity:  100.00%     Mismatches:    0
Query Match:            100.00%     Indels:        0
DB:                     14          Gaps:          0

US-10-066-521-6 (1-1344) x US-10-124-498-5 (1-4035)

Qy          1 MetGluGlyAspLysSerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysLysSerSerGluSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy         41 ThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy         61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy         81 AsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspAspMetLysLysIleSerGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300

Qy        101 AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGluIleSerGlnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360

Qy        121 MetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGlyHisGlyGlyAspThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420

Qy        141 TrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspValArgArgSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480

Qy        161 PheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540

Qy        181 AspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGlyIleGlyLys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600

Qy        201 SerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGlyLeuTyrGlnGlyMet 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660

Qy        221 PheSerTyrValPhePheLeuProValArgGluMetGlnArgLysLysGluSerSerVal 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720

Qy        241 ThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMetSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780

Qy        261 ArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsn 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840

Qy        281 AsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProProPheThrLeuIleArg 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900

Qy        301 SerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrValArgAspVal 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960

Qy        321 GlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuValArgGlyIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020

Qy        341 SerGlyGluGlnArgIleHisLeuLeuGluArgGlyIleGlyGluHisGlnLysThr 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080

Qy        361 GlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAla 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140

Qy        381 ValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyGluSerValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200

Qy        401 ProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrPro 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260

Qy        421 ArgGlyValValArgArgCysLeuAsnLeuGluGluArgValValLeuLysArgPheCys 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320

Qy        441 ArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyAspAspLeuMet 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380

Qy        461 ValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuPro 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440

Qy        481 AspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAla 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500

Qy        501 AlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeuCysProLeuTyrVal 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560

Qy        521 GluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620

Qy        541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680

Qy        561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeu 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740

Qy        581 GlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeuPhe 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800

Qy        601 GluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrpLeu 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860

Qy        621 ProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyr 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920

Qy        641 LeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerAlaGluAla 660

Db       1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980

Qy        661 CysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrpGluAsp 680

Db       1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040

Qy        681 PheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIle 700

Db       2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100

Qy        701 LeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCysLysIle 720

Db       2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160

Qy        721 GlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrpArgIle 740

Db       2161 CAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATC 2220

Qy        741 ValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGluGlu 760

Db       2221 GTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAG 2280

Qy        761 AspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSerLeuArg 780

Db       2281 GATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGG 2340

Qy        781 LeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThrThr 800

Db       2341 CTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACC 2400

Qy        801 SerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMet 820

Db       2401 TCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATG 2460

Qy        821 ProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAsp 840

Db       2461 CCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGAC 2520

Qy        841 CysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSer 860

Db       2521 TGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGC 2580

Qy        861 LeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeuCys 880

Db       2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640

Qy        881 ArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeu 900

Db       2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700

Qy        901 AspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHis 920

Db       2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760

Qy        921 LeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGluValMet 940

Db       2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820

Qy        941 ArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThrAlaAla 960

Db       2821 AGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCG 2880

Qy        961 CysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAspLeu 980

Db       2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940

Qy        981 ThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGlnLys 1000

Db       2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000

Qy       1001 AsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCysGlu 1020

Db       3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060

Qy       1021 AlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGlnAsn 1040

Db       3061 GCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAAT 3120

Qy       1041 AsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSerAsn 1060

Db       3121 AACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAAC 3180

Qy       1061 LeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleArgLysLeuGluGlu 1080

Db       3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240

Qy       1081 GluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHisSerPheAspGlu 1100

Db       3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300

Qy       1101 AspAspArgHisLysIleGlyLeuThrPheArgLeuProGluSerArgAlaTrpProCys 1120

Db       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360

Qy       1121 AlaLeuLeuTrpGlyMetAsnProGluGlnLysLysArgValSerLeuLeuAlaGlyAsp 1140

Db       3361 GCCTTGCTGTGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420

Qy       1141 PheLysSerSerThrArgPheAlaLysSerLeuCysLeuAlaThrAlaAsnGlyGluSer 1160

Db       3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480

Qy       1161 GlnArgValAspAsnValGluGlnSerSerProGlnProMetAlaGlyThrGluHisLys 1180

Db       3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540

Qy       1181 GlnAspLysMetLeuSerValGlyTyrSerGlyAlaTrpSerGluThrAlaGluLeuGlu 1200

Db       3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600

Qy       1201 GlyLeuGlySerAsnSerAlaAspHisAspHisGlyGlyMetAlaTrpSerLeuGlyArg 1220

Db       3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660

Qy       1221 GluLeuSerSerArgGlyLeuCysProThrValLeuMetThrThrAlaValCysProGly 1240

Db       3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720

Qy       1241 HisTrpGluArgLeuGlySerArgGlyTrpCysLeuAsnSerAlaAspAspHisSerGly 1260

Db       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780

Qy       1261 ValSerTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuValSerAsnSerAlaAspAsp 1280

Db       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840

Qy       1281 HisSerGlyValAlaTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuValSerAsnSer 1300

Db       3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900

Qy       1301 AlaAspAspHisSerGlyValSerTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuVal 1320

Db       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960

Qy       1321 SerAsnSerAlaAspAspHisSerGlyValSerTrpSerLeuGlyAlaAlaGlyLeuGlu 1340

Db       3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020

Qy       1341 GlyLeuValSer 1344

Db       4021 GGGCTGGTGTCT 4032
```

```
RESULT 2
US-10-066-521-5
; Sequence 5, Application US/10066521
; Publication No. US20030027757A1
; GENERAL INFORMATION:
;  APPLICANT: Bertin, John
;  APPLICANT:  Wang, Weiye
;  APPLICANT:  Blatcher, Maria
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
;  TITLE OF INVENTION:  PROTEIN FAMILY AND USES THEREOF
;  FILE REFERENCE: 07334-334001
;  CURRENT APPLICATION NUMBER: US/10/066,521
;  CURRENT FILING DATE:  2002-06-25
;  PRIOR APPLICATION NUMBER: 60/318,645
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: 60/265,231
;  PRIOR FILING DATE: 2001-01-31
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 4035
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(4032)
US-10-066-521-5

Alignment Scores:
Pred. No.:              0              Length:         4035
Score:                  1344.00        Matches:        1344
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     14             Gaps:           0

US-10-066-521-6 (1-1344) x US-10-066-521-5 (1-4035)

Qy          1 MetGluGlyAspLysSerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysLysSerSerGluSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy         41 ThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy         61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy         81 AsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspAspMetLysLysIleSerGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300

Qy        101 AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGluIleSerGlnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360

Qy        121 MetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGlyHisGlyGlyAspThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420

Qy        141 TrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspValArgArgSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480

Qy        161 PheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540

Qy        181 AspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGlyIleGlyLys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600

Qy        201 SerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGlyLeuTyrGlnGlyMet 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660

Qy        221 PheSerTyrValPhePheLeuProValArgGluMetGlnArgLysLysGluSerServal 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720

Qy        241 ThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMetSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780

Qy        261 ArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsn 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840

Qy        281 AsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProProPheThrLeuIleArg 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900

Qy        301 SerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrValArgAspVal 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960

Qy        321 GlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuValArgGlyIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020

Qy        341 SerGlyGluGlnArgIleHisLeuLeuLeuGluArgGlyIleGlyGluHisGlnLysThr 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080

Qy        361 GlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAla 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140

Qy        381 ValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyGluSerValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200

Qy        401 ProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrPro 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260

Qy        421 ArgGlyValValArgArgCysLeuAsnLeuGluGluArgValValLeuLysArgPheCys 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320

Qy        441 ArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyAspAspLeuMet 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380

Qy        461 ValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuPro 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440

Qy        481 AspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAla 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500

Qy        501 AlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeuCysProLeuTyrVal 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560

Qy        521 GluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620
```

```
Qy       541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560
Db      1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680

Qy       561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeu 580
Db      1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740

Qy       581 GlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeuPhe 600
Db      1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800

Qy       601 GluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrpLeu 620
Db      1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860

Qy       621 ProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyr 640
Db      1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920

Qy       641 LeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerAlaGluAla 660
Db      1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980

Qy       661 CysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrpGluAsp 680
Db      1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040

Qy       681 PheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIle 700
Db      2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100

Qy       701 LeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCysLysIle 720
Db      2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160

Qy       721 GlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrpArgIle 740
Db      2161 CAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATC 2220

Qy       741 ValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGluGlu 760
Db      2221 GTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAG 2280

Qy       761 AspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSerLeuArg 780
Db      2281 GATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGG 2340

Qy       781 LeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThrThr 800
Db      2341 CTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACC 2400

Qy       801 SerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMet 820
Db      2401 TCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATG 2460

Qy       821 ProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAsp 840
Db      2461 CCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGAC 2520

Qy       841 CysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSer 860
Db      2521 TGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGC 2580

Qy       861 LeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeuCys 880
Db      2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640

Qy       881 ArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeu 900
Db      2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700

Qy       901 AspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHis 920
```

```
Db      2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760

Qy       921 LeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGluValMet 940
Db      2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820

Qy       941 ArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThrAlaAla 960
Db      2821 AGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCG 2880

Qy       961 CysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAspLeu 980
Db      2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940

Qy       981 ThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGlnLys 1000
Db      2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000

Qy      1001 AsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCysGlu 1020
Db      3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060

Qy      1021 AlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGlnAsn 1040
Db      3061 GCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAAT 3120

Qy      1041 AsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSerAsn 1060
Db      3121 AACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAAC 3180

Qy      1061 LeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleArgLysLeuLeuGlu 1080
Db      3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240

Qy      1081 GluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHisSerPheAspGlu 1100
Db      3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300

Qy      1101 AspAspArgHisLysIleGlyLeuThrPheArgLeuProGluSerArgAlaTrpProCys 1120
Db      3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360

Qy      1121 AlaLeuLeuTrpGlyMetAsnProGluGlnLysLysArgValSerLeuLeuAlaGlyAsp 1140
Db      3361 GCCTTGCTGTGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420

Qy      1141 PheLysSerSerThrArgPheAlaLysSerLeuCysLeuAlaThrAlaAsnGlyGluSer 1160
Db      3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480

Qy      1161 GlnArgValAspAsnValGluGlnSerSerProGlnProMetAlaGlyThrGluHisLys 1180
Db      3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540

Qy      1181 GlnAspLysMetLeuSerValGlyTyrSerGlyAlaTrpSerGluThrAlaGluLeuGlu 1200
Db      3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600

Qy      1201 GlyLeuGlySerAsnSerAlaAspHisAspHisGlyGlyMetAlaTrpSerLeuGlyArg 1220
Db      3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660

Qy      1221 GluLeuSerSerArgGlyLeuCysProThrValLeuMetThrThrAlaValCysProGly 1240
Db      3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720

Qy      1241 HisTrpGluArgLeuGlySerArgGlyTrpCysLeuAsnSerAlaAspAspHisSerGly 1260
Db      3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780

Qy      1261 ValSerTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuValSerAsnSerAlaAspAsp 1280
```

```
Db       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840

Qy       1281 HisSerGlyValAlaTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuValSerAsnSer 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900

Qy       1301 AlaAspAspHisSerGlyValSerTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuVal 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960

Qy       1321 SerAsnSerAlaAspAspHisSerGlyValSerTrpSerLeuGlyAlaAlaGlyLeuGlu 1340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020

Qy       1341 GlyLeuValSer 1344
              ||||||||||||
Db       4021 GGGCTGGTGTCT 4032

RESULT 3
US-10-416-642-3
; Sequence 3, Application US/10416642
; Publication No. US20040043452A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  ARVIZU, Chandra
;  TITLE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS
;  FILE REFERENCE: PF-0842 PCT
;  CURRENT APPLICATION NUMBER: US/10/416,642
;  CURRENT FILING DATE:  2003-05-13
;  PRIOR APPLICATION NUMBER: 60/249,407
;  PRIOR FILING DATE: 2000-11-15
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PERL Program
; SEQ ID NO 3
;   LENGTH: 3489
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040043452A1 7474830CB1
US-10-416-642-3

Alignment Scores:
Pred. No.:              0           Length:         3489
Score:                  1006.00     Matches:        1006
Percent Similarity:     100.00%     Conservative:   0
Best Local Similarity:  100.00%     Mismatches:     0
Query Match:            74.85%      Indels:         0
DB:                     17          Gaps:           0

US-10-066-521-6 (1-1344) x US-10-416-642-3 (1-3489)

Qy         98 IleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGluIle 117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 ATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATT 513

Qy        118 SerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGlyHisGly 137
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 TCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGA 573

Qy        138 GlyAspThrTrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspVal 157
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTA 633

Qy        158 ArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAla 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 CGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCT 693

Qy        178 PheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGly 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 TTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGA 753

Qy        198 IleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGlyLeuTyr 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 ATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTAC 813

Qy        218 GlnGlyMetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLysLysGlu 237
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 CAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAG 873

Qy        238 SerSerValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGlu 257
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAG 933

Qy        258 IleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySer 277
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCT 993

Qy        278 ValLeuAsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProProPheThr 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 GTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACC 1053

Qy        298 LeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrVal 317
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 CTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTC 1113

Qy        318 ArgAspValGlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuVal 337
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTT 1173

Qy        338 ArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGluArgGlyIleGlyGluHis 357
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 AGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCAT 1233

Qy        358 GlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGln 377
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 CAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAG 1293

Qy        378 ValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyGlu 397
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAG 1353

Qy        398 SerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGln 417
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 AGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAG 1413

Qy        418 LeuThrProArgGlyValValArgArgCysLeuAsnLeuGluGluArgValValLeuLys 437
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 CTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAG 1473

Qy        438 ArgPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyAsp 457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 CGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGACGGTGAC 1533

Qy        458 AspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsnIle 477
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 GACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATC 1593

Qy        478 LeuLeuProAspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeuGlnAsp 497
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 CTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGAC 1653

Qy        498 PheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeuCysPro 517
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 TTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCT 1713

Qy        518 LeuTyrValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHis 537
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 CTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCAC 1773

Qy        538 SerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeu 557
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 TCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTG 1833

Qy        558 GluValLeuLeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpVal 577
```

```
Db       1834 GAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTC 1893

Qy        578 SerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHis 597

Db       1894 TCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCAC 1953

Qy        598 CysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGlu 617

Db       1954 TGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAA 2013

Qy        618 ValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHis 637

Db       2014 GTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCAC 2073

Qy        638 CysProTyrLeuArgLysIleArgValAspValLysGlyIleProProArgAspGluSer 657

Db       2074 TGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCC 2133

Qy        658 AlaGluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGln 677

Db       2134 GCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAG 2193

Qy        678 TrpGluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGly 697

Db       2194 TGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGC 2253

Qy        698 SerSerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThr 717

Db       2254 AGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACC 2313

Qy        718 CysLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeu 737

Db       2314 TGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTC 2373

Qy        738 TrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeu 757

Db       2374 TGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTG 2433

Qy        758 LysGluGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGlu 777

Db       2434 AAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAG 2493

Qy        778 SerLeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIle 797

Db       2494 TCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATC 2553

Qy        798 LeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGln 817

Db       2554 CTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAG 2613

Qy        818 GlyValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIle 837

Db       2614 GGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATA 2673

Qy        838 LeuGluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSer 857

Db       2674 CTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGC 2733

Qy        858 AsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsn 877

Db       2734 AACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAAT 2793

Qy        878 LeuLeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGln 897

Db       2794 CTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAG 2853

Qy        898 CysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrp 917

Db       2854 TGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGG 2913

Qy        918 LeuThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCys 937

Db       2914 CTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGC 2973

Qy        938 GluValMetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeu 957

Db       2974 GAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTC 3033

Qy        958 ThrAlaAlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSer 977

Db       3034 ACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGC 3093

Qy        978 LeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeu 997

Db       3094 CTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAGGGACTG 3153

Qy        998 LysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAsp 1017

Db       3154 AAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGAT 3213

Qy       1018 CysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeu 1037

Db       3214 TGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTG 3273

Qy       1038 ValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysPro 1057

Db       3274 GTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCC 3333

Qy       1058 ThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleArgLys 1077

Db       3334 ACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAG 3393

Qy       1078 LeuLeuGluGluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHisSer 1097

Db       3394 CTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCT 3453

Qy       1098 PheAspGluAspAspArg 1103

Db       3454 TTTGATGAAGATGACCGG 3471
```

RESULT 4
US-10-216-645-1
; Sequence 1, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; APPLICANT: LESSL, MONIKA
; APPLICANT: PETERS-KOTTIG, MICHAELE
; APPLICANT: BECKMANN, GEORG
; TITLE OF INVENTION: HUMAN MATER PROTEINS
; FILE REFERENCE: SCH-1910
; CURRENT APPLICATION NUMBER: US/10/216,645
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-216-645-1

Alignment Scores:

Pred. No.:	0	Length:	3926
Score:	1006.00	Matches:	1006
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	74.85%	Indels:	0
DB:	15	Gaps:	0

US-10-066-521-6 (1-1344) x US-10-216-645-1 (1-3926)

```
Qy         98 IleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGluIle 117
```

```
Db        454 ATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATT 513

Qy        118 SerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGlyHisGly 137

Db        514 TCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGA 573

Qy        138 GlyAspThrTrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspVal 157

Db        574 GGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTA 633

Qy        158 ArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAla 177

Db        634 CGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCT 693

Qy        178 PheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGly 197

Db        694 TTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGA 753

Qy        198 IleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGlyLeuTyr 217

Db        754 ATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTAC 813

Qy        218 GlnGlyMetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLysLysGlu 237

Db        814 CAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAG 873

Qy        238 SerSerValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGlu 257

Db        874 AGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAG 933

Qy        258 IleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySer 277

Db        934 ATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCT 993

Qy        278 ValLeuAsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProProPheThr 297

Db        994 GTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACC 1053

Qy        298 LeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrVal 317

Db       1054 CTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTC 1113

Qy        318 ArgAspValGlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuVal 337

Db       1114 AGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTT 1173

Qy        338 ArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGluArgGlyIleGlyGluHis 357

Db       1174 AGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCAT 1233

Qy        358 GlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGln 377

Db       1234 CAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAG 1293

Qy        378 ValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyGlu 397

Db       1294 GTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAG 1353

Qy        398 SerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGln 417

Db       1354 AGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAG 1413

Qy        418 LeuThrProArgGlyValValArgArgCysLeuAsnLeuGluGluArgValValLeuLys 437

Db       1414 CTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAG 1473

Qy        438 ArgPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyAsp 457

Db       1474 CGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGACGGTGAC 1533

Qy        458 AspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsnIle 477

Db       1534 GACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATC 1593

Qy        478 LeuLeuProAspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeuGlnAsp 497

Db       1594 CTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGAC 1653

Qy        498 PheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeuCysPro 517

Db       1654 TTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCT 1713

Qy        518 LeuTyrValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHis 537

Db       1714 CTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCAC 1773

Qy        538 SerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeu 557

Db       1774 TCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTG 1833

Qy        558 GluValLeuLeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpVal 577

Db       1834 GAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTC 1893

Qy        578 SerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHis 597

Db       1894 TCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCAC 1953

Qy        598 CysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGlu 617

Db       1954 TGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAA 2013

Qy        618 ValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHis 637

Db       2014 GTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCAC 2073

Qy        638 CysProTyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSer 657

Db       2074 TGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCC 2133

Qy        658 AlaGluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGln 677

Db       2134 GCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAG 2193

Qy        678 TrpGluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGly 697

Db       2194 TGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGC 2253

Qy        698 SerSerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThr 717

Db       2254 AGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACC 2313

Qy        718 CysLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeu 737

Db       2314 TGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTC 2373

Qy        738 TrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeu 757

Db       2374 TGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTG 2433

Qy        758 LysGluGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGlu 777

Db       2434 AAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAG 2493

Qy        778 SerLeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIle 797

Db       2494 TCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATC 2553

Qy        798 LeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGln 817

Db       2554 CTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAG 2613

Qy        818 GlyValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIle 837

Db       2614 GGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATA 2673
```

```
Qy        838 LeuGluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSer 857
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 CTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGC 2733

Qy        858 AsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsn 877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2734 AACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAAT 2793

Qy        878 LeuLeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGln 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2794 CTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAG 2853

Qy        898 CysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrp 917
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2854 TGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGG 2913

Qy        918 LeuThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCys 937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2914 CTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGC 2973

Qy        938 GluValMetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeu 957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2974 GAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTC 3033

Qy        958 ThrAlaAlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSer 977
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3034 ACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGC 3093

Qy        978 LeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeu 997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3094 CTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAGGGACTG 3153

Qy        998 LysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAsp 1017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 AAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGAT 3213

Qy       1018 CysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeu 1037
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3214 TGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTG 3273

Qy       1038 ValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysPro 1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3274 GTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCC 3333

Qy       1058 ThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleArgLys 1077
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3334 ACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAG 3393

Qy       1078 LeuLeuGluGluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHisSer 1097
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3394 CTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCT 3453

Qy       1098 PheAspGluAspAspArg 1103
              |||||||||||||||||
Db       3454 TTTGATGAAGATGACCGG 3471

RESULT 5
US-10-216-645-3
; Sequence 3, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
;  APPLICANT: WEISS, BERTRAM
;  APPLICANT:  LESSL, MONIKA
;  APPLICANT:  PETERS-KOTTIG, MICHAELE
;  APPLICANT:  BECKMANN, GEORG
;  TITLE OF INVENTION: HUMAN MATER PROTEINS
;  FILE REFERENCE: SCH-1910
;  CURRENT APPLICATION NUMBER: US/10/216,645
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 3830
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-216-645-3

Alignment Scores:
Pred. No.:                0          Length:          3830
Score:                    988.00     Matches:         988
Percent Similarity:       100.00%    Conservative:    0
Best Local Similarity:    100.00%    Mismatches:      0
Query Match:              73.51%     Indels:          0
DB:                       15         Gaps:            0

US-10-066-521-6 (1-1344) x US-10-216-645-3 (1-3830)

Qy        116 GluIleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGly 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GAAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGA 510

Qy        136 HisGlyGlyAspThrTrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGlu 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 CATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAG 570

Qy        156 AspValArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAla 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 GATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCT 630

Qy        176 GlyAlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLys 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 GGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAG 690

Qy        196 SerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGly 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 TCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGA 750

Qy        216 LeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLys 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 CTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAG 810

Qy        236 LysGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProVal 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 AAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTG 870

Qy        256 ThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 ACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTG 930

Qy        276 GlySerValLeuAsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProPro 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 GGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCG 990

Qy        296 PheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleVal 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 TTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTC 1050

Qy        316 ThrValArgAspValGlyThrGluLysLeuLysSerGluValValSerProArgTyrLeu 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 ACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTG 1110

Qy        336 LeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuGluArgGlyIleGly 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 TTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGT 1170

Qy        356 GluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGln 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAG 1230

Qy        376 CysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValVal 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 TGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTG 1290

Qy        396 GlyGluSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPhe 415
```

```
Db       1291 GGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTT 1350

Qy        416 HisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGluGluArgValVal 435

Db       1351 CATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTC 1410

Qy        436 LeuLysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAsp 455

Db       1411 CTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGAC 1470

Qy        456 GlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMet 475

Db       1471 GGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATG 1530

Qy        476 AsnIleLeuLeuProAspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeu 495

Db       1531 AACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTC 1590

Qy        496 GlnAspPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeu 515

Db       1591 CAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTC 1650

Qy        516 CysProLeuTyrValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHis 535

Db       1651 TGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCAT 1710

Qy        536 IleHisSerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGluAspValArgArg 555

Db       1711 ATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGG 1770

Qy        556 ProLeuGluValLeuLeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHis 575

Db       1771 CCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCAC 1830

Qy        576 TrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAla 595

Db       1831 TGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCC 1890

Qy        596 PheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPhe 615

Db       1891 TTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTC 1950

Qy        616 GlnGluValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeu 635

Db       1951 CAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTC 2010

Qy        636 GlnHisCysProTyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAsp 655

Db       2011 CAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGAT 2070

Qy        656 GluSerAlaGluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGlu 675

Db       2071 GAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAG 2130

Qy        676 GluGlnTrpGluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAsp 695

Db       2131 GAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGAC 2190

Qy        696 LeuGlySerSerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHis 715

Db       2191 CTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCAT 2250

Qy        716 ProThrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGln 735

Db       2251 CCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAG 2310

Qy        736 HisLeuTrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThr 755

Db       2311 CACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACC 2370

Qy        756 HisLeuLysGluGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeu 775

Db       2371 CACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTG 2430

Qy        776 LeuGluSerLeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSer 795

Db       2431 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2490

Qy        796 GlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThr 815

Db       2491 CAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACA 2550

Qy        816 AspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLys 835

Db       2551 GACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAG 2610

Qy        836 LeuIleLeuGluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeu 855

Db       2611 CTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTC 2670

Qy        856 ValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGly 875

Db       2671 GTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGT 2730

Qy        876 ValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeu 895

Db       2731 GTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTG 2790

Qy        896 AsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsn 915

Db       2791 AATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAAC 2850

Qy        916 SerTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeu 935

Db       2851 TCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTT 2910

Qy        936 LeuCysGluValMetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCys 955

Db       2911 CTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGT 2970

Qy        956 HisLeuThrAlaAlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeu 975

Db       2971 CATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTG 3030

Qy        976 LysSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGlu 995

Db       3031 AAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAG 3090

Qy        996 GlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThr 1015

Db       3091 GGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACT 3150

Qy       1016 SerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeu 1035

Db       3151 TCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTA 3210

Qy       1036 AsnLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAla 1055

Db       3211 AACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCC 3270

Qy       1056 CysProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIle 1075

Db       3271 TGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATA 3330

Qy       1076 ArgLysLeuLeuGluGluValGlnLeuLeuLysProArgValValIleAspGlySerTrp 1095

Db       3331 AGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGG 3390

Qy       1096 HisSerPheAspGluAspAspArg 1103

Db       3391 CATTCTTTTGATGAAGATGACCGG 3414
```

RESULT 6
US-10-092-900A-347
; Sequence 347, Application US/10092900A

```
; Publication No. US20040043382A1
; GENERAL INFORMATION:
;  APPLICANT: Padigaru, Muralidhara
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Taupier Jr., Raymond J.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Li, Li
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Ji, Weizhen
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Guo, Xiaojia Sasha
;  APPLICANT:  Tchernev,, Velizar T.
;  APPLICANT:  Fernandes, Elma R.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Liu, Yi
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Catterton, Elina
;  APPLICANT:  Leite, Mario W.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Alsobrook, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-290C
;  CURRENT APPLICATION NUMBER: US/10/092,900A
;  CURRENT FILING DATE:  2002-03-07
;  PRIOR APPLICATION NUMBER: USSN 60/274,322
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/283,675
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: USSN 60/338,092
;  PRIOR FILING DATE: 2001-12-03
;  PRIOR APPLICATION NUMBER: USSN 60/274,281
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/274,191
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/325,681
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: USSN 60/304,354
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: USSN 60/279,995
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: USSN 60/294,899
;  PRIOR FILING DATE: 2001-05-31
;  PRIOR APPLICATION NUMBER: USSN 60/287,424
;  PRIOR FILING DATE: 2001-04-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 347
;   LENGTH: 3226
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (69)..(3168)
US-10-092-900A-347

Alignment Scores:
Pred. No.:              0           Length:        3226
Score:                  968.00      Matches:       968
Percent Similarity:     100.00%     Conservative:  0
Best Local Similarity:  100.00%     Mismatches:    0

Query Match:            72.02%      Indels:        0
DB:                     17          Gaps:          0

US-10-066-521-6 (1-1344) x US-10-092-900A-347 (1-3226)

Qy        136 HisGlyGlyAspThrTrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGlu 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 CATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAG 308

Qy        156 AspValArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAla 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCT 368

Qy        176 GlyAlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLys 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAG 428

Qy        196 SerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGly 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGA 488

Qy        216 LeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLys 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAG 548

Qy        236 LysGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProVal 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 AAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTG 608

Qy        256 ThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 ACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTG 668

Qy        276 GlySerValLeuAsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProPro 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCG 728

Qy        296 PheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleVal 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTC 788

Qy        316 ThrValArgAspValGlyThrGluLysLeuLysSerGluValValSerProArgTyrLeu 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 ACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTG 848

Qy        336 LeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGluArgGlyIleGly 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 TTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGT 908

Qy        356 GluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGln 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 GAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAG 968

Qy        376 CysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValVal 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 TGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTG 1028

Qy        396 GlyGluSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPhe 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1029 GGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTT 1088

Qy        416 HisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGluGluArgValVal 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 CATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTC 1148

Qy        436 LeuLysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAsp 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1149 CTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGAC 1208

Qy        456 GlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMet 475
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1209 GGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATG 1268
```

```
Qy       476 AsnIleLeuLeuProAspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeu 495
Db      1269 AACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTC 1328

Qy       496 GlnAspPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeu 515
Db      1329 CAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTC 1388

Qy       516 CysProLeuTyrValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHis 535
Db      1389 TGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCAT 1448

Qy       536 IleHisSerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGluAspValArgArg 555
Db      1449 ATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGG 1508

Qy       556 ProLeuGluValLeuLeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHis 575
Db      1509 CCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCAC 1568

Qy       576 TrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAla 595
Db      1569 TGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCC 1628

Qy       596 PheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPhe 615
Db      1629 TTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTC 1688

Qy       616 GlnGluValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeu 635
Db      1689 CAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTC 1748

Qy       636 GlnHisCysProTyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAsp 655
Db      1749 CAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGAT 1808

Qy       656 GluSerAlaGluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGlu 675
Db      1809 GAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAG 1868

Qy       676 GluGlnTrpGluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAsp 695
Db      1869 GAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGAC 1928

Qy       696 LeuGlySerSerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHis 715
Db      1929 CTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCAT 1988

Qy       716 ProThrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGln 735
Db      1989 CCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAG 2048

Qy       736 HisLeuTrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThr 755
Db      2049 CACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACC 2108

Qy       756 HisLeuLysGluGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeu 775
Db      2109 CACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTG 2168

Qy       776 LeuGluSerLeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSer 795
Db      2169 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2228

Qy       796 GlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThr 815
Db      2229 CAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACA 2288

Qy       816 AspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLys 835
Db      2289 GACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAG 2348

Qy       836 LeuIleLeuGluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeu 855
Db      2349 CTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTC 2408

Qy       856 ValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGly 875
Db      2409 GTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGT 2468

Qy       876 ValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeu 895
Db      2469 GTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTG 2528

Qy       896 AsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsn 915
Db      2529 AATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAAC 2588

Qy       916 SerTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeu 935
Db      2589 TCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTT 2648

Qy       936 LeuCysGluValMetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCys 955
Db      2649 CTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGT 2708

Qy       956 HisLeuThrAlaAlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeu 975
Db      2709 CATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTG 2768

Qy       976 LysSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGlu 995
Db      2769 AAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAG 2828

Qy       996 GlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThr 1015
Db      2829 GGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACT 2888

Qy      1016 SerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeu 1035
Db      2889 TCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTA 2948

Qy      1036 AsnLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAla 1055
Db      2949 AACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCC 3008

Qy      1056 CysProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIle 1075
Db      3009 TGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATA 3068

Qy      1076 ArgLysLeuLeuGluGluValGlnLeuLeuLysProArgValValIleAspGlySerTrp 1095
Db      3069 AGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGG 3128

Qy      1096 HisSerPheAspGluAspAspArg 1103
Db      3129 CATTCTTTTGATGAAGATGACCGG 3152

RESULT 7
US-10-860-761-3
; Sequence 3, Application US/10860761
; Publication No. US20040248775A1
; GENERAL INFORMATION:
;  APPLICANT: WYETH
;  TITLE OF INVENTION: METHODS FOR SCREENING INHIBITORS OF APOPTOSIS
;  FILE REFERENCE: AM101318
;  CURRENT APPLICATION NUMBER: US/10/860,761
;  CURRENT FILING DATE:  2004-06-03
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 3885
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
```

; LOCATION: (1)..(3603)
US-10-860-761-3

Alignment Scores:

Pred. No.:	0	Length:	3885
Score:	616.00	Matches:	1002
Percent Similarity:	99.21%	Conservative:	0
Best Local Similarity:	99.21%	Mismatches:	4
Query Match:	45.83%	Indels:	8
DB:	18	Gaps:	0

US-10-066-521-6 (1-1344) x US-10-860-761-3 (1-3885)

```
Qy         98 IleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGluIle 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 ATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATT 627

Qy        118 SerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGlyHisGly 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 TCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGA 687

Qy        138 GlyAspThrTrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspVal 157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 GGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTA 747

Qy        158 ArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAla 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        748 CGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCT 807

Qy        178 PheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGly 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 TTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGA 867

Qy        198 IleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGlyLeuTyr 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        868 ATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTAC 927

Qy        218 GlnGlyMetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLysLysGlu 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 CAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAG 987

Qy        238 SerSerValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGlu 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        988 AGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAG 1047

Qy        258 IleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySer 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1048 ATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCT 1107

Qy        278 ValLeuAsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProProPheThr 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1108 GTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACC 1167

Qy        298 LeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrVal 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 CTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTC 1227

Qy        318 ArgAspValGlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuVal 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1228 AGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTT 1287

Qy        338 ArgGlyIleSerGlyGluGlnArgIleHisLeuLeuGluArgGlyIleGlyGluHis 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1288 AGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCAT 1347

Qy        358 GlnLysThrGlnGlyLeuArgAlaIleMet-AsnAsnArgGluLeuLeuAspGlnCysGl 377
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db       1348 CAGAAGACACAAGGGTTGCGTGCGATCAT-CAACAACCGTGAGCTGCTCGACCAGTGCCA 1406

Qy        377 nValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyGl 397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1407 GGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGA 1466

Qy        397 uSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheVal-PheHisG 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    |||||||
Db       1467 GAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGC-GTTTCATC 1525

Qy        417 lnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGluGluArgValValLeuL 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1526 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 1585

Qy        437 ysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyA 457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1586 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTG 1645

Qy        457 spAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsnI 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1646 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 1705

Qy        477 leLeuLeuProAspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeuGlnA 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1706 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1765

Qy        497 spPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeuCysP 517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1766 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1825

Qy        517 roLeuTyrValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleH 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1826 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1885

Qy        537 isSerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProL 557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1886 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1945

Qy        557 euGluValLeuLeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpV 577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1946 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 2005

Qy        577 alSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheH 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2006 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 2065

Qy        597 isCysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnG 617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2066 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 2125

Qy        617 luValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnH 637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2126 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 2185

Qy        637 isCysProTyrLeuArgLysIleArgValAspValLysGlyIleProArgAspGluS 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2186 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 2245

Qy        657 erAlaGluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluG 677
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2246 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2305

Qy        677 lnTrpGluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuG 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2306 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2365

Qy        697 lySerSerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProT 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2366 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2425

Qy        717 hrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisL 737
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2426 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACC 2485

Qy        737 euTrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisL 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2486 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2545

Qy        757 euLysGluGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuG 777
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2546 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2605

Qy         777 luSerLeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnI 797
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2606 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2665

Qy         797 leLeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspG 817
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2666 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2725

Qy         817 lnGlyValMet-ProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeu 836
                ||||||||    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2726 AGGGAGTAAC-GCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTG 2784

Qy         837 IleLeuGluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuVal 856
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2785 ATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTC 2844

Qy         857 SerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyVal 876
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2845 AGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTA 2904

Qy         877 AsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsn 896
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2905 AATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAAT 2964

Qy         897 GlnCysHisLeuAspThrAlaGlyCysGlyPhe-LeuAlaLeuAlaLeuMetGlyAsnSe 916
                ||||||||||||||||||||||||||    ||| ||||||||||||||||||||||||||||||
Db        2965 CAGTGCCACCTGGACACGGCTGGCTGTGG-TTCTCTTGCACTTGCGCTTATGGGTAACTC 3023

Qy         916 rTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLe 936
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3024 ATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCT 3083

Qy         936 uCysGluValMetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHi 956
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3084 GTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCA 3143

Qy         956 sLeuThrAlaAlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLy 976
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3144 TCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAA 3203

Qy         976 sSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGl 996
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3204 GAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGG 3263

Qy         996 yLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSe 1016
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3264 ACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTC 3323

Qy        1016 rAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAs 1036
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3324 TGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAA 3383

Qy        1036 nLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCy 1056
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3384 CCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTG 3443

Qy        1056 sProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleAr 1076
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3444 TCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAG 3503

Qy        1076 gLysLeuLeuGluGluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHi 1096
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3504 GAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCA 3563

Qy        1096 sSerPheAspGluAspAspArg 1103
                |||||||||||||||||||||
Db        3564 TTCTTTTGATGAAGATGACCGG 3585

RESULT 8
US-10-399-443-23
```

```
; Sequence 23, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as Represented by the
;  APPLICANT:  Secretary, Department of Health & Human Services, The National Institute
;  APPLICANT:  Health
;  APPLICANT:  Nelson, Lawrence M.
;  APPLICANT:  Tong, Zhi-Bin
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Zhi-Bin, Tong
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64785
;  CURRENT APPLICATION NUMBER: US/10/399,443
;  CURRENT FILING DATE:  2003-04-16
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
;   LENGTH: 3900
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3600)
;   OTHER INFORMATION:
US-10-399-443-23

Alignment Scores:
Pred. No.:              0               Length:         3900
Score:                  616.00          Matches:        1002
Percent Similarity:     99.21%          Conservative:   0
Best Local Similarity:  99.21%          Mismatches:     4
Query Match:            45.83%          Indels:         8
DB:                     17              Gaps:           0

US-10-066-521-6 (1-1344) x US-10-399-443-23 (1-3900)

Qy          98 IleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGluIle 117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         568 ATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATT 627

Qy         118 SerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGlyHisGly 137
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         628 TCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGA 687

Qy         138 GlyAspThrTrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspVal 157
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         688 GGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTA 747

Qy         158 ArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAla 177
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         748 CGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCT 807

Qy         178 PheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGly 197
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         808 TTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGA 867

Qy         198 IleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGlyLeuTyr 217
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         868 ATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTAC 927

Qy         218 GlnGlyMetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLysLysGlu 237
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         928 CAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAG 987

Qy         238 SerSerValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGlu 257
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         988 AGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAG 1047

Qy         258 IleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySer 277
```

```
Db      1048 ATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCT 1107

Qy       278 ValLeuAsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProProPheThr 297

Db      1108 GTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACC 1167

Qy       298 LeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrVal 317

Db      1168 CTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTC 1227

Qy       318 ArgAspValGlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuVal 337

Db      1228 AGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTT 1287

Qy       338 ArgGlyIleSerGlyGluGlnArgIleHisLeuLeuGluArgGlyIleGlyGluHis 357

Db      1288 AGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCAT 1347

Qy       358 GlnLysThrGlnGlyLeuArgAlaIleMet-AsnAsnArgGluLeuLeuAspGlnCysGl 377

Db      1348 CAGAAGACACAAGGGTTGCGTGCGATCAT-CAACAACCGTGAGCTGCTCGACCAGTGCCA 1406

Qy       377 nValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyGl 397

Db      1407 GGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGA 1466

Qy       397 uSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheVal-PheHisG 417

Db      1467 GAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGC-GTTTCATC 1525

Qy       417 lnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGluGluArgValValLeuL 437

Db      1526 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 1585

Qy       437 ysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyA 457

Db      1586 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTG 1645

Qy       457 spAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsnI 477

Db      1646 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 1705

Qy       477 leLeuLeuProAspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeuGlnA 497

Db      1706 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1765

Qy       497 spPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeuCysP 517

Db      1766 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1825

Qy       517 roLeuTyrValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleH 537

Db      1826 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1885

Qy       537 isSerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProL 557

Db      1886 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1945

Qy       557 euGluValLeuLeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpV 577

Db      1946 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 2005

Qy       577 alSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheH 597

Db      2006 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 2065

Qy       597 isCysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnG 617

Db      2066 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 2125

Qy       617 luValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnH 637

Db      2126 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 2185

Qy       637 isCysProTyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluS 657

Db      2186 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 2245

Qy       657 erAlaGluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluG 677

Db      2246 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2305

Qy       677 lnTrpGluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuG 697

Db      2306 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2365

Qy       697 lySerSerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProT 717

Db      2366 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2425

Qy       717 hrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisL 737

Db      2426 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACC 2485

Qy       737 euTrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisL 757

Db      2486 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2545

Qy       757 euLysGluGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuG 777

Db      2546 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2605

Qy       777 luSerLeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnI 797

Db      2606 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2665

Qy       797 leLeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspG 817

Db      2666 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2725

Qy       817 lnGlyValMet-ProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeu 836

Db      2726 AGGGAGTAAC-GCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTG 2784

Qy       837 IleLeuGluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuVal 856

Db      2785 ATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTC 2844

Qy       857 SerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyVal 876

Db      2845 AGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTA 2904

Qy       877 AsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsn 896

Db      2905 AATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAAT 2964

Qy       897 GlnCysHisLeuAspThrAlaGlyCysGlyPhe-LeuAlaLeuAlaLeuMetGlyAsnSe 916

Db      2965 CAGTGCCACCTGGACACGGCTGGCTGTGG-TTCTCTTGCACTTGCGCTTATGGGTAACTC 3023

Qy       916 rTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLe 936

Db      3024 ATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCT 3083

Qy       936 uCysGluValMetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHi 956

Db      3084 GTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCA 3143

Qy       956 sLeuThrAlaAlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLy 976

Db      3144 TCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAA 3203

Qy       976 sSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGl 996

Db      3204 GAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGG 3263
```

```
Qy       996 yLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSe 1016
Db      3264 ACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTC 3323

Qy      1016 rAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAs 1036
Db      3324 TGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAA 3383

Qy      1036 nLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCy 1056
Db      3384 CCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTG 3443

Qy      1056 sProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleAr 1076
Db      3444 TCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAG 3503

Qy      1076 gLysLeuLeuGluGluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHi 1096
Db      3504 GAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCA 3563

Qy      1096 sSerPheAspGluAspAspArg 1103
Db      3564 TTCTTTTGATGAAGATGACCGG 3585

RESULT 9
US-10-677-943-23
; Sequence 23, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
;   LENGTH: 3900
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3600)
US-10-677-943-23

Alignment Scores:
Pred. No.:              0           Length:         3900
Score:                  616.00      Matches:        1002
Percent Similarity:     99.21%      Conservative:   0
Best Local Similarity:  99.21%      Mismatches:     4
Query Match:            45.83%      Indels:         8
DB:                     17          Gaps:           0

US-10-066-521-6 (1-1344) x US-10-677-943-23 (1-3900)

Qy        98 IleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGluIle 117
Db       568 ATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATT 627

Qy       118 SerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGlyHisGly 137
Db       628 TCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGA 687

Qy       138 GlyAspThrTrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspVal 157
Db       688 GGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTA 747

Qy       158 ArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAla 177
Db       748 CGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCT 807

Qy       178 PheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGly 197
Db       808 TTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGA 867

Qy       198 IleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGlyLeuTyr 217
Db       868 ATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTAC 927

Qy       218 GlnGlyMetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLysLysGlu 237
Db       928 CAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAG 987

Qy       238 SerSerValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGlu 257
Db       988 AGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAG 1047

Qy       258 IleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySer 277
Db      1048 ATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCT 1107

Qy       278 ValLeuAsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProProPheThr 297
Db      1108 GTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACC 1167

Qy       298 LeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrVal 317
Db      1168 CTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTC 1227

Qy       318 ArgAspValGlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuVal 337
Db      1228 AGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTT 1287

Qy       338 ArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGluArgGlyIleGlyGluHis 357
Db      1288 AGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCAT 1347

Qy       358 GlnLysThrGlnGlyLeuArgAlaIleMet-AsnAsnArgGluLeuLeuAspGlnCysGl 377
Db      1348 CAGAAGACACAAGGGTTGCGTGCGATCAT-CAACAACCGTGAGCTGCTCGACCAGTGCCA 1406

Qy       377 nValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyGl 397
Db      1407 GGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGA 1466

Qy       397 uSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheVal-PheHisG 417
Db      1467 GAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGC-GTTTCATC 1525

Qy       417 lnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGluGluArgValValLeuL 437
Db      1526 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 1585

Qy       437 ysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyA 457
Db      1586 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTG 1645

Qy       457 spAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsnI 477
Db      1646 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 1705

Qy       477 leLeuLeuProAspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeuGlnA 497
Db      1706 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1765
```

```
Qy       497 spPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeuCysP 517
Db      1766 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1825

Qy       517 roLeuTyrValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleH 537
Db      1826 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1885

Qy       537 isSerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProL 557
Db      1886 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1945

Qy       557 euGluValLeuLeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpV 577
Db      1946 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 2005

Qy       577 alSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheH 597
Db      2006 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 2065

Qy       597 isCysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnG 617
Db      2066 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 2125

Qy       617 luValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnH 637
Db      2126 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 2185

Qy       637 isCysProTyrLeuArgLysIleArgValAspValLysGlyIleProArgAspGluS 657
Db      2186 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 2245

Qy       657 erAlaGluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluG 677
Db      2246 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2305

Qy       677 lnTrpGluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuG 697
Db      2306 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2365

Qy       697 lySerSerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProT 717
Db      2366 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2425

Qy       717 hrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisL 737
Db      2426 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACC 2485

Qy       737 euTrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisL 757
Db      2486 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2545

Qy       757 euLysGluGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuG 777
Db      2546 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2605

Qy       777 luSerLeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnI 797
Db      2606 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2665

Qy       797 leLeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspG 817
Db      2666 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2725

Qy       817 lnGlyValMet-ProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeu 836
Db      2726 AGGGAGTAAC-GCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTG 2784

Qy       837 IleLeuGluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuVal 856
Db      2785 ATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTC 2844

Qy       857 SerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyVal 876
Db      2845 AGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTA 2904

Qy       877 AsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsn 896
Db      2905 AATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAAT 2964

Qy       897 GlnCysHisLeuAspThrAlaGlyCysGlyPhe-LeuAlaLeuAlaLeuMetGlyAsnSe 916
Db      2965 CAGTGCCACCTGGACACGGCTGGCTGTGG-TTCTCTTGCACTTGCGCTTATGGGTAACTC 3023

Qy       916 rTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLe 936
Db      3024 ATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCT 3083

Qy       936 uCysGluValMetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHi 956
Db      3084 GTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCA 3143

Qy       956 sLeuThrAlaAlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLy 976
Db      3144 TCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAA 3203

Qy       976 sSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGl 996
Db      3204 GAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGG 3263

Qy       996 yLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSe 1016
Db      3264 ACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTC 3323

Qy      1016 rAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAs 1036
Db      3324 TGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAA 3383

Qy      1036 nLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCy 1056
Db      3384 CCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTG 3443

Qy      1056 sProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleAr 1076
Db      3444 TCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAG 3503

Qy      1076 gLysLeuLeuGluGluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHi 1096
Db      3504 GAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCA 3563

Qy      1096 sSerPheAspGluAspAspArg 1103
Db      3564 TTCTTTTGATGAAGATGACCGG 3585
```

RESULT 10
US-10-399-443-1
; Sequence 1, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1

```
; SEQ ID NO 1
;   LENGTH: 1157
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-399-443-1

Alignment Scores:
Pred. No.:              0              Length:         1157
Score:                  385.00         Matches:        385
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            28.65%         Indels:         0
DB:                     17             Gaps:           0

US-10-066-521-6 (1-1344) x US-10-399-443-1 (1-1157)

Qy        252 GlnAlaProValThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGly 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAAGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGT 60

Qy        272 PheAspAspLeuGlySerValLeuAsnAsnAspThrLysLeuCysLysAspTrpAlaGlu 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAG 120

Qy        292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSer 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCC 180

Qy        312 PheLeuIleValThrValArgAspValGlyThrGluLysLeuLysSerGluValValSer 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCT 240

Qy        332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGlu 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAG 300

Qy        352 ArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGlu 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAG 360

Qy        372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTG 420

Qy        392 GlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAla 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCC 480

Qy        412 AlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGlu 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAG 540

Qy        432 GluArgValValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLys 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAG 600

Qy        452 SerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAla 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCT 660

Qy        472 LeuPheHisMetAsnIleLeuLeuProAspSerHisCysGluGluTyrTyrThrPhePhe 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTC 720

Qy        492 HisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluIle 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATC 780

Qy        512 GluProAlaLeuCysProLeuTyrValGluLysThrLysArgSerMetGluLeuLysGln 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAG 840

Qy        532 AlaGlyPheHisIleHisSerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGlu 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAA 900

Qy        552 AspValArgArgProLeuGluValLeuLeuGlyCysProValProLeuGlyValLysGln 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAG 960

Qy        572 LysLeuLeuHisTrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAsp 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGAC 1020

Qy        592 ThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAla 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCA 1080

Qy        612 LeuAsnSerPheGlnGluValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSer 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCT 1140

Qy        632 SerPheCysLeuGln 636
              |||||||||||||||
Db       1141 TCCTTCTGCCTCCAG 1155

RESULT 11
US-10-677-943-1
; Sequence 1, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 1157
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-677-943-1

Alignment Scores:
Pred. No.:              0              Length:         1157
Score:                  385.00         Matches:        385
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            28.65%         Indels:         0
DB:                     17             Gaps:           0

US-10-066-521-6 (1-1344) x US-10-677-943-1 (1-1157)

Qy        252 GlnAlaProValThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGly 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAAGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGT 60

Qy        272 PheAspAspLeuGlySerValLeuAsnAsnAspThrLysLeuCysLysAspTrpAlaGlu 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAG 120

Qy        292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSer 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCC 180
```

```
Qy        312 PheLeuIleValThrValArgAspValGlyThrGluLysLeuLysSerGluValValSer 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCT 240

Qy        332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGlu 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAG 300

Qy        352 ArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGlu 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAG 360

Qy        372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTG 420

Qy        392 GlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAla 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCC 480

Qy        412 AlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGlu 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAG 540

Qy        432 GluArgValValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLys 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAG 600

Qy        452 SerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAla 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCT 660

Qy        472 LeuPheHisMetAsnIleLeuLeuProAspSerHisCysGluGluTyrTyrThrPhePhe 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTC 720

Qy        492 HisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluIle 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATC 780

Qy        512 GluProAlaLeuCysProLeuTyrValGluLysThrLysArgSerMetGluLeuLysGln 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAG 840

Qy        532 AlaGlyPheHisIleHisSerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGlu 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAA 900

Qy        552 AspValArgArgProLeuGluValLeuLeuGlyCysProValProLeuGlyValLysGln 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAG 960

Qy        572 LysLeuLeuHisTrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAsp 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGAC 1020

Qy        592 ThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAla 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCA 1080

Qy        612 LeuAsnSerPheGlnGluValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSer 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCT 1140

Qy        632 SerPheCysLeuGln 636
              ||||||||||||||||
Db       1141 TCCTTCTGCCTCCAG 1155

RESULT 12
US-10-399-443-3
; Sequence 3, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as Represented by the
;  APPLICANT:  Secretary, Department of Health & Human Services, The National Institute
;  APPLICANT:  Health
;  APPLICANT:  Nelson, Lawrence M.
;  APPLICANT:  Tong, Zhi-Bin
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Zhi-Bin, Tong
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64785
;  CURRENT APPLICATION NUMBER: US/10/399,443
;  CURRENT FILING DATE:  2003-04-16
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 1075
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-399-443-3

Alignment Scores:
Pred. No.:              1.19e-192       Length:         1075
Score:                  196.00          Matches:        252
Percent Similarity:     99.21%          Conservative:   0
Best Local Similarity:  99.21%          Mismatches:     1
Query Match:            14.58%          Indels:         2
DB:                     17              Gaps:           0

US-10-066-521-6 (1-1344) x US-10-399-443-3 (1-1075)

Qy        851 LeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSer 870
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGC 61

Qy        871 LeuGlyAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeu 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTG 121

Qy        891 GlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPhe-LeuAlaLe 910
              |||||||||||||||||||||||||||||||||||||||||||||   ||| ||||||||
Db        122 CAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGG-TTCTCTTGCACT 180

Qy        910 uAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAs 930
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 240

Qy        930 pAsnGlyValLysLeuLeuCysGluValMetArgGluProSerCysHisLeuGlnAspLe 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 300

Qy        950 uGluLeuValLysCysHisLeuThrAlaAlaCysCysGluSerLeuSerCysValIleSe 970
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAGTTGGTAAAATGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 360

Qy        970 rArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyVa 990
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 420

Qy        990 lAlaAlaLeuCysGluGlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLy 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 480

Qy       1010 sAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnAr 1030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 540

Qy       1030 gHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLe 1050
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 600
```

```
Qy       1050 uCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGl 1070
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 660

Qy       1070 nTyrProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuLysProArgValVa 1090
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 720

Qy       1090 lIleAspGlySerTrpHisSerPheAspGluAspAspArg 1103
             |||||||||||||||||||||||||||||||||||||
Db        721 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGG 760

RESULT 13
US-10-677-943-3
; Sequence 3, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 1075
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-677-943-3

Alignment Scores:
Pred. No.:              1.19e-192       Length:         1075
Score:                  196.00          Matches:        252
Percent Similarity:     99.21%          Conservative:   0
Best Local Similarity:  99.21%          Mismatches:     1
Query Match:            14.58%          Indels:         2
DB:                     17              Gaps:           0

US-10-066-521-6 (1-1344) x US-10-677-943-3 (1-1075)

Qy        851 LeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSer 870
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGC 61

Qy        871 LeuGlyAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeu 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTG 121

Qy        891 GlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPhe-LeuAlaLe 910
              ||||||||||||||||||||||||||||||||||||||||||||||   ||| ||||||||
Db        122 CAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGG-TTCTCTTGCACT 180

Qy        910 uAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAs 930
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 240

Qy        930 pAsnGlyValLysLeuLeuCysGluValMetArgGluProSerCysHisLeuGlnAspLe 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 300

Qy        950 uGluLeuValLysCysHisLeuThrAlaAlaCysCysGluSerLeuSerCysValIleSe 970
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAGTTGGTAAAATGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 360

Qy        970 rArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyVa 990
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 420

Qy        990 lAlaAlaLeuCysGluGlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLy 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 480

Qy       1010 sAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnAr 1030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 540

Qy       1030 gHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLe 1050
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 600

Qy       1050 uCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGl 1070
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 660

Qy       1070 nTyrProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuLysProArgValVa 1090
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 720

Qy       1090 lIleAspGlySerTrpHisSerPheAspGluAspAspArg 1103
             |||||||||||||||||||||||||||||||||||||
Db        721 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGG 760

RESULT 14
US-10-027-632-258159
; Sequence 258159, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 258159
;   LENGTH: 2099
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-258159

Alignment Scores:
Pred. No.:              3.52e-48        Length:         2099
Score:                  57.00           Matches:        57
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            4.24%           Indels:         0
DB:                     13              Gaps:           0

US-10-066-521-6 (1-1344) x US-10-027-632-258159 (1-2099)

Qy        668 MetArgAspLysThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGlyThr 687
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 ATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACC 279

Qy        688 HisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLys 707
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 CACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAG 339

Qy        708 ThrLeuCysAlaLysLeuArgHisProThrCysLysIleGlnThrLeuMet 724
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 ACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATG 390

RESULT 15
US-10-027-632-258159
; Sequence 258159, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 258159
;   LENGTH: 2099
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-258159

Alignment Scores:
Pred. No.:              3.52e-48        Length:         2099
Score:                  57.00           Matches:        57
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            4.24%           Indels:         0
DB:                     17              Gaps:           0

US-10-066-521-6 (1-1344) x US-10-027-632-258159 (1-2099)

Qy        668 MetArgAspLysThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGlyThr 687
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 ATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACC 279

Qy        688 HisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLys 707
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 CACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAG 339

Qy        708 ThrLeuCysAlaLysLeuArgHisProThrCysLysIleGlnThrLeuMet 724
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 ACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATG 390


Search completed: February  5, 2005, 01:22:59
Job time : 1727 secs
```

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 4, 2005, 13:10:24 ; Search time 496 Seconds
(without alignments)
4433.782 Million cell updates/sec

Title: US-10-066-521-6
Perfect score: 7074
Sequence: 1 MEGDKSLTFSSYGLQWCLYE.....DDHSGVSWSLGAAGLEGLVS 1344

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10066521/runat_04022005_114552_4412/app_query.fasta_1.1543
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=std.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10066521_@CGN_1_1_107_@runat_04022005_114552_4412 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	955	13.5	4422	4	US-09-388-221B-1	Sequence 1, Appli
2	949	13.4	4200	4	US-09-388-221B-3	Sequence 3, Appli
3	949	13.4	4332	4	US-09-388-221B-5	Sequence 5, Appli
4	948	13.4	4466	4	US-09-388-221B-11	Sequence 11, Appl
5	945.5	13.4	4556	4	US-09-388-221B-9	Sequence 9, Appli
6	630.5	8.9	1374	2	US-08-910-731-3	Sequence 3, Appli
7	630.5	8.9	1374	2	US-08-795-395-3	Sequence 3, Appli
8	621	8.8	1371	2	US-08-910-731-1	Sequence 1, Appli
9	621	8.8	1371	2	US-08-795-395-1	Sequence 1, Appli
10	612	8.7	1371	2	US-08-910-731-7	Sequence 7, Appli
11	607.5	8.6	1386	2	US-08-910-731-5	Sequence 5, Appli
12	406	5.7	3156	4	US-09-799-451-870	Sequence 870, App
13	379.5	5.4	4141	3	US-09-245-281-42	Sequence 42, Appl
14	379.5	5.4	4141	3	US-09-207-359B-42	Sequence 42, Appl
15	379.5	5.4	4141	4	US-09-340-620A-42	Sequence 42, Appl
16	379.5	5.4	4141	4	US-09-865-364-42	Sequence 42, Appl
17	364	5.1	4485	4	US-09-949-016-3209	Sequence 3209, Ap
18	364	5.1	4485	4	US-10-014-269-1	Sequence 1, Appli
19	359.5	5.1	3382	3	US-09-099-041A-7	Sequence 7, Appli
20	359.5	5.1	3382	3	US-09-245-281-7	Sequence 7, Appli
21	359.5	5.1	3382	3	US-09-207-359B-7	Sequence 7, Appli
22	359.5	5.1	3382	4	US-09-340-620A-7	Sequence 7, Appli
23	359.5	5.1	3382	4	US-09-865-364-7	Sequence 7, Appli
24	351	5.0	4486	4	US-10-014-269-33	Sequence 33, Appl
25	347	4.9	2859	3	US-09-099-041A-9	Sequence 9, Appli
26	347	4.9	2859	3	US-09-245-281-9	Sequence 9, Appli
27	347	4.9	2859	3	US-09-207-359B-9	Sequence 9, Appli
28	347	4.9	2859	4	US-09-340-620A-9	Sequence 9, Appli
29	347	4.9	2859	4	US-09-865-364-9	Sequence 9, Appli
30	327	4.6	4543	2	US-08-519-547A-5	Sequence 5, Appli
31	319.5	4.5	4346	4	US-09-064-199-12	Sequence 12, Appl
32	319.5	4.5	4366	4	US-09-064-199-14	Sequence 14, Appl
33	319.5	4.5	4418	4	US-09-064-199-13	Sequence 13, Appl
34	319.5	4.5	4431	4	US-09-064-199-8	Sequence 8, Appli
35	319.5	4.5	4441	3	US-09-641-999-2	Sequence 2, Appli
36	319.5	4.5	4441	4	US-09-064-199-10	Sequence 10, Appl
37	319.5	4.5	4549	4	US-09-064-199-9	Sequence 9, Appli
38	319.5	4.5	4564	4	US-09-064-199-2	Sequence 2, Appli
39	319.5	4.5	4649	4	US-09-064-199-11	Sequence 11, Appl
40	319.5	4.5	4746	4	US-09-064-199-7	Sequence 7, Appli
41	319.5	4.5	5105	4	US-09-064-199-3	Sequence 3, Appli
42	319.5	4.5	5463	4	US-09-064-199-1	Sequence 1, Appli
43	309	4.4	3393	1	US-08-295-502-1	Sequence 1, Appli
44	309	4.4	3393	5	PCT-US95-10691-1	Sequence 1, Appli
45	307	4.3	4302	3	US-09-245-281-38	Sequence 38, Appl

ALIGNMENTS

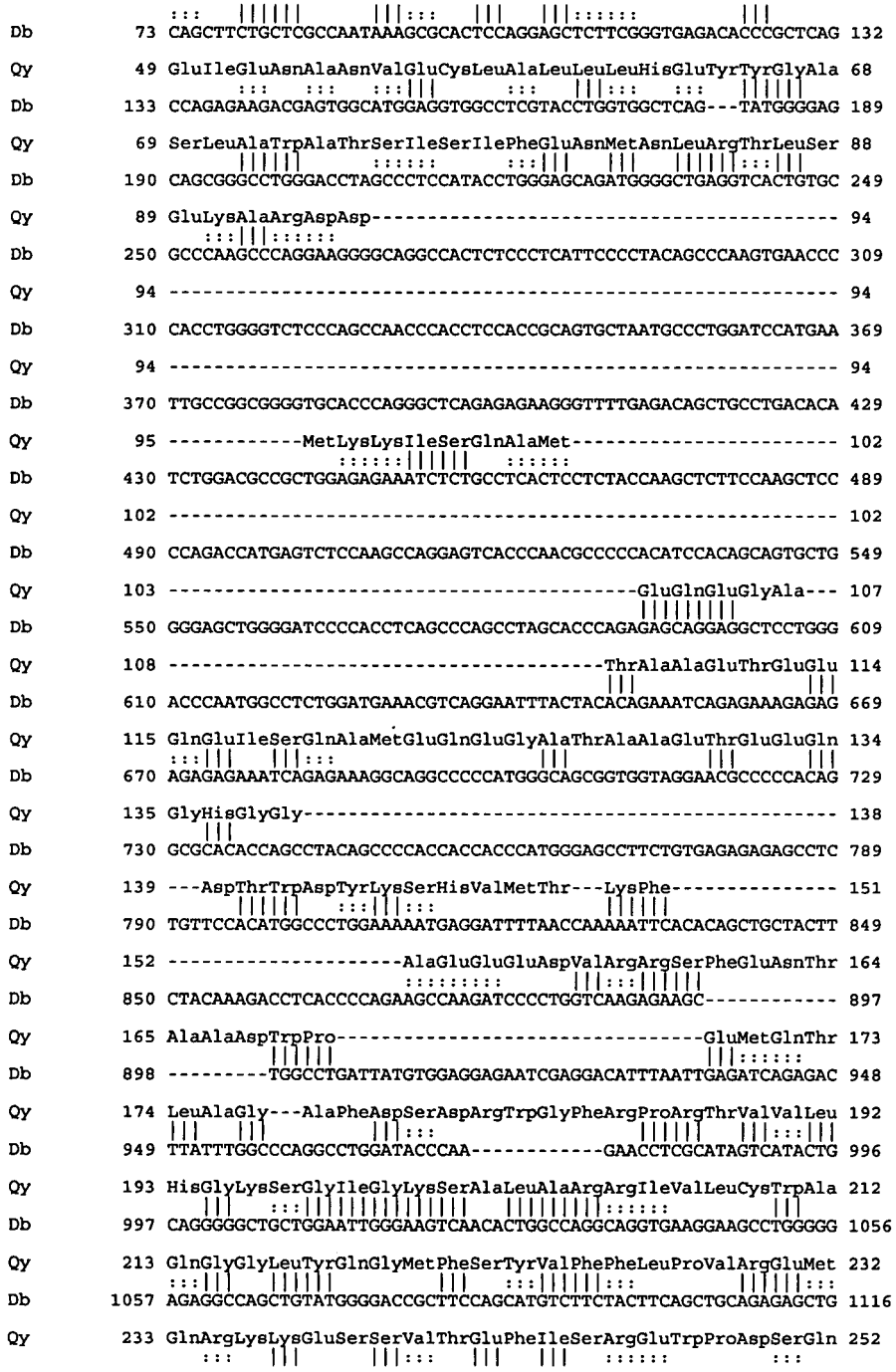
RESULT 1
US-09-388-221B-1
; Sequence 1, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4422
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4422)
US-09-388-221B-1

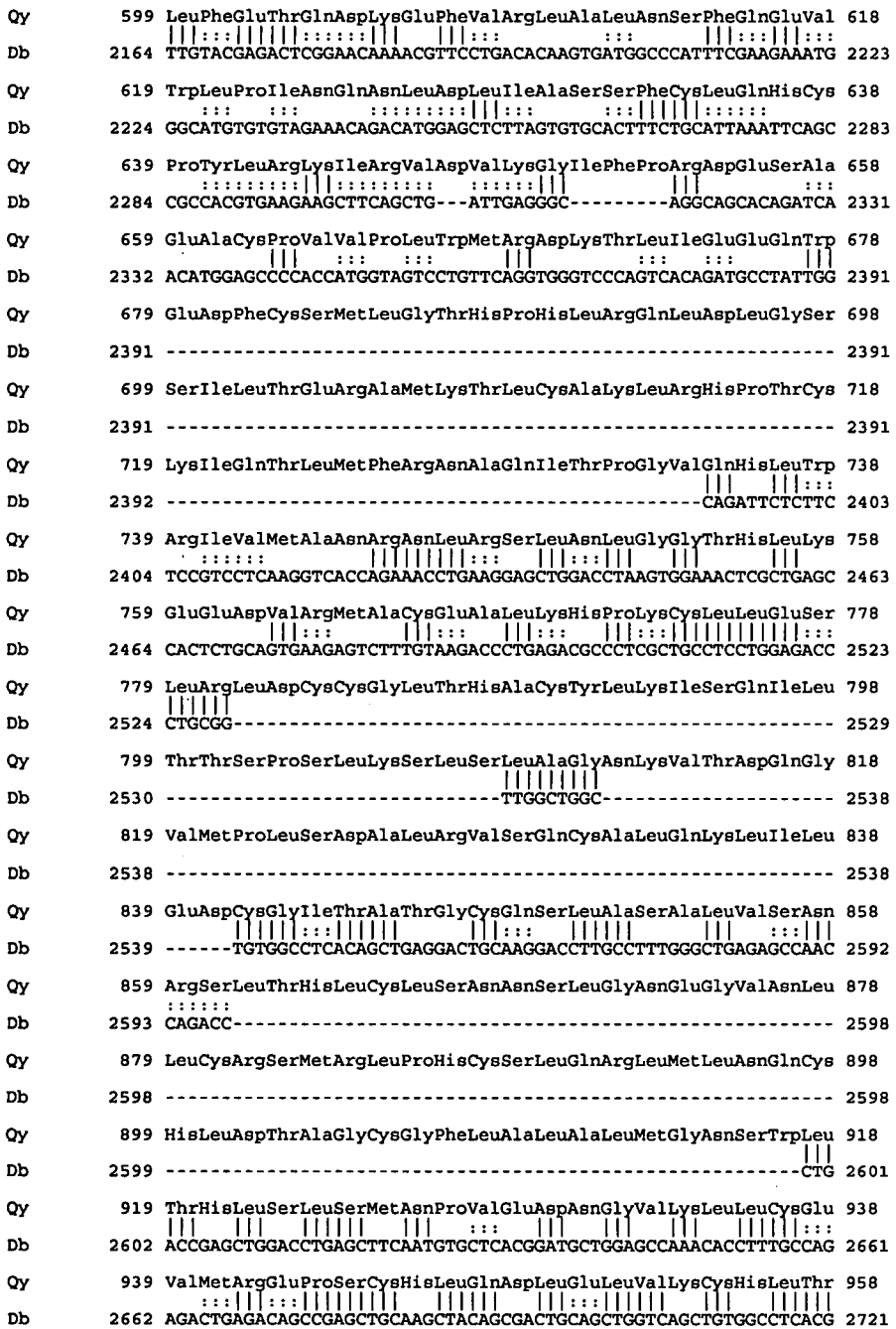
Alignment Scores:

Pred. No.:	4.57e-91	Length:	4422
Score:	955.00	Matches:	366
Percent Similarity:	38.01%	Conservative:	189
Best Local Similarity:	25.07%	Mismatches:	438
Query Match:	13.50%	Indels:	468
DB:	4	Gaps:	51

US-10-066-521-6 (1-1344) x US-09-388-221B-1 (1-4422)

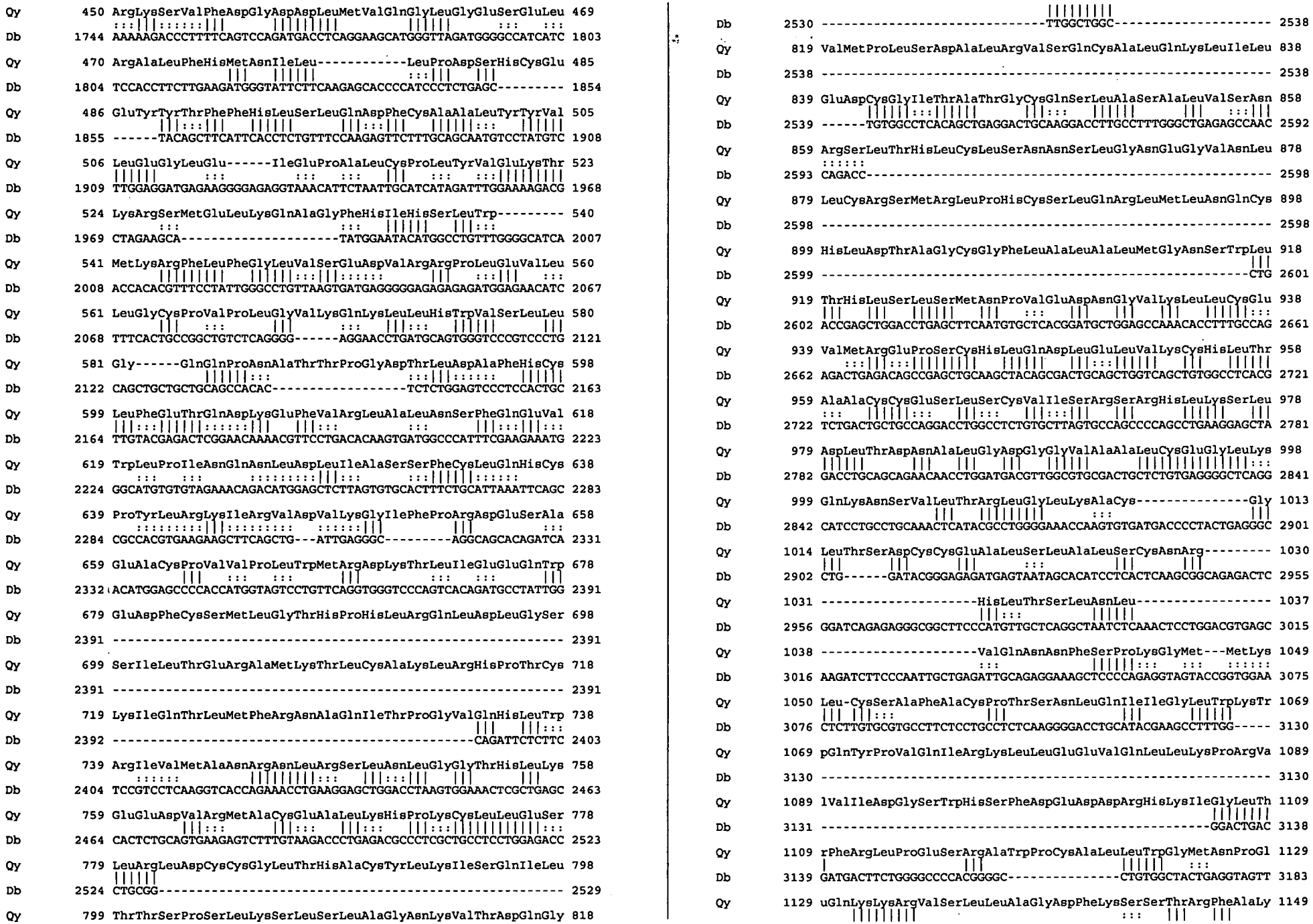
```
Qy          11 SerTyrGlyLeuGlnTrpCysLeuTyrGlu---LeuAspLysGluGluPheGlnThrPhe 29
               ::::::|||          |||      |||  |||  |||||||||   :::   |||
Db          13 GCCTGGGGCCGCCTGGCCTGTTACTTGGAGTTCCTGAAGAAGGAGGAGCTGAAGGAGTTC 72

Qy          30 LysGluLeuLeuLysLysLysSer---SerGluSerThrThrCysSerIleProGlnPhe 48
```


Db 73 CAGCTTCTGCTCGCCAATAAAGCGCACTCCAGGAGCTCTTCGGGTGAGACACCCGCTCAG 132
Qy 49 GluIleGluAsnAlaAsnValGluCysLeuAlaLeuLeuLeuHisGluTyrTyrGlyAla 68
Db 133 CCAGAGAAGACGAGTGGCATGGAGGTGGCCTCGTACCTGGTGGCTCAG---TATGGGGAG 189
Qy 69 SerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArgThrLeuSer 88
Db 190 CAGCGGGCCTGGGACCTAGCCCTCCATACCTGGGAGCAGATGGGGCTGAGGTCACTGTGC 249
Qy 89 GluLysAlaArgAspAsp---------- 94
Db 250 GCCCAAGCCCAGGAAGGGGCAGGCCACTCTCCCTCATTCCCCTACAGCCCAAGTGAACCC 309
Qy 94 ---------- 94
Db 310 CACCTGGGGTCTCCCAGCCAACCCACCTCCACCGCAGTGCTAATGCCCTGGATCCATGAA 369
Qy 94 ---------- 94
Db 370 TTGCCGGCGGGGTGCACCCAGGGCTCAGAGAGAAGGGTTTTGAGACAGCTGCCTGACACA 429
Qy 95 ----------MetLysLysIleSerGlnAlaMet---------- 102
Db 430 TCTGGACGCCGCTGGAGAGAAATCTCTGCCTCACTCCTCTACCAAGCTCTTCCAAGCTCC 489
Qy 102 ---------- 102
Db 490 CCAGACCATGAGTCTCCAAGCCAGGAGTCACCCAACGCCCCCACATCCACAGCAGTGCTG 549
Qy 103 ----------GluGlnGluGlyAla--- 107
Db 550 GGGAGCTGGGGATCCCCACCTCAGCCCAGCCTAGCACCCAGAGAGCAGGAGGCTCCTGGG 609
Qy 108 ----------ThrAlaAlaGluThrGluGlu 114
Db 610 ACCCAATGGCCTCTGGATGAAACGTCAGGAATTTACTACACAGAAATCAGAGAAAGAGAG 669
Qy 115 GlnGluIleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGln 134
Db 670 AGAGAGAAATCAGAGAAAGGCAGGCCCCCATGGGCAGCGGTGGTAGGAACGCCCCCACAG 729
Qy 135 GlyHisGlyGly---------- 138
Db 730 GCGCACACCAGCCTACAGCCCCACCACCACCCATGGGAGCCTTCTGTGAGAGAGAGCCTC 789
Qy 139 ---AspThrTrpAspTyrLysSerHisValMetThr---LysPhe---------- 151
Db 790 TGTTCCACATGGCCCTGGAAAAATGAGGATTTTAACCAAAAATTCACACAGCTGCTACTT 849
Qy 152 ----------AlaGluGluGluAspValArgArgSerPheGluAsnThr 164
Db 850 CTACAAAGACCTCACCCCAGAAGCCAAGATCCCCTGGTCAAGAGAAGC---------- 897
Qy 165 AlaAlaAspTrpPro----------GluMetGlnThr 173
Db 898 ---------TGGCCTGATTATGTGGAGGAGAATCGAGGACATTTAATTGAGATCAGAGAC 948
Qy 174 LeuAlaGly---AlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeu 192
Db 949 TTATTTGGCCCAGGCCTGGATACCCAA----------GAACCTCGCATAGTCATACTG 996
Qy 193 HisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAla 212
Db 997 CAGGGGGCTGCTGGAATTGGGAAGTCAACACTGGCCAGGCAGGTGAAGGAAGCCTGGGGG 1056
Qy 213 GlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMet 232
Db 1057 AGAGGCCAGCTGTATGGGGACCGCTTCCAGCATGTCTTCTACTTCAGCTGCAGAGAGCTG 1116
Qy 233 GlnArgLysLysGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGln 252
Db 1117 GCCCAGTCCAAGGTGGTGAGTCTCGCTGAGCTCATCGGAAAAGATGGGACAGCCACTCCG 1176
Qy 253 AlaProValThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPhe 272
Db 1177 GCTCCCATTAGACAGATCCTGTCTAGGCCAGAGCGGCTGCTCTTCATCCTCGATGGTGTA 1236
Qy 273 AspAspLeuGlySerValLeuAsnAsn---AspThrLysLeuCysLysAspTrpAlaGlu 291
Db 1237 GATGAGCCAGGATGGGTCTTGCAGGAGCCGAGTTCTGAGCTCTGTCTGCACTGGAGCCAG 1296
Qy 292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSer 311
Db 1297 CCACAGCCGGCGGATGCACTGCTGGGCAGTTTGCTGGGGAAAACTATACTTCCCGAGGCA 1356
Qy 312 PheLeuIleValThrValArgAspValGlyThrGluLysLeuLysSerGluValValSer 331
Db 1357 TCCTTCCTGATCACGGCTCGGACCACAGCTCTGCAGAACCTCATTCCTTCTTTGGAGCAG 1416
Qy 332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGlu 351
Db 1417 GCACGTTGGGTAGAGGTCCTGGGGTTCTCTGAGTCCAGCAGGAAGGAATATTTCTACAGA 1476
Qy 352 ArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGlu 371
Db 1477 TATTTCACAGATGAAAGGCAAGCAATTAGAGCCTTTAGGTTGGTCAAATCAAACAAAGAG 1536
Qy 372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu 391
Db 1537 CTCTGGGCCCTGTGTCTTGTGCCCTGGGTGTCCTGGCTGGCCTGCACTTGCCTGATGCAG 1596
Qy 392 GlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeuThrGly------Leu 409
Db 1597 CAGATGAAGCGGAAGGAAAAACTCACACTGACTTCCAAGACCACCACAACCCTCTGTCTA 1656
Qy 410 HisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsn 429
Db 1657 CATTACCTTGCCCAGGCTCTCCAAGCTCAGCCATTGGGA---------- 1695
Qy 430 LeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsn 449
Db 1696 ----------CCCCAGCTCAGAGACCTCTGCTCTCTGGCTGCTGAGGGCATCTGGCAA 1743
Qy 450 ArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeu 469
Db 1744 AAAAAGACCCTTTTCAGTCCAGATGACCTCAGGAAGCATGGGTTAGATGGGGCCATCATC 1803
Qy 470 ArgAlaLeuPheHisMetAsnIleLeu----------LeuProAspSerHisCysGlu 485
Db 1804 TCCACCTTCTTGAAGATGGGTATTCTTCAAGAGCACCCCATCCCTCTGAGC--------- 1854
Qy 486 GluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrVal 505
Db 1855 ------TACAGCTTCATTCACCTCTGTTTCCAAGAGTTCTTTGCAGCAATGTCCTATGTC 1908
Qy 506 LeuGluGlyLeuGlu------IleGluProAlaLeuCysProLeuTyrValGluLysThr 523
Db 1909 TTGGAGGATGAGAAGGGGAGAGGTAAACATTCTAATTGCATCATAGATTTGGAAAAGACG 1968
Qy 524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp--------- 540
Db 1969 CTAGAAGCA----------TATGGAATACATGGCCTGTTTGGGGCATCA 2007
Qy 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560
Db 2008 ACCACACGTTTCCTATTGGGCCTGTTAAGTGATGAGGGGGAGAGAGAGATGGAGAACATC 2067
Qy 561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeu 580
Db 2068 TTTCACTGCCGGCTGTCTCAGGGG------AGGAACCTGATGCAGTGGGTCCCGTCCCTG 2121
Qy 581 Gly------GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCys 598
Db 2122 CAGCTGCTGCTGCAGCCACAC----------TCTCTGGAGTCCCTCCACTGC 2163

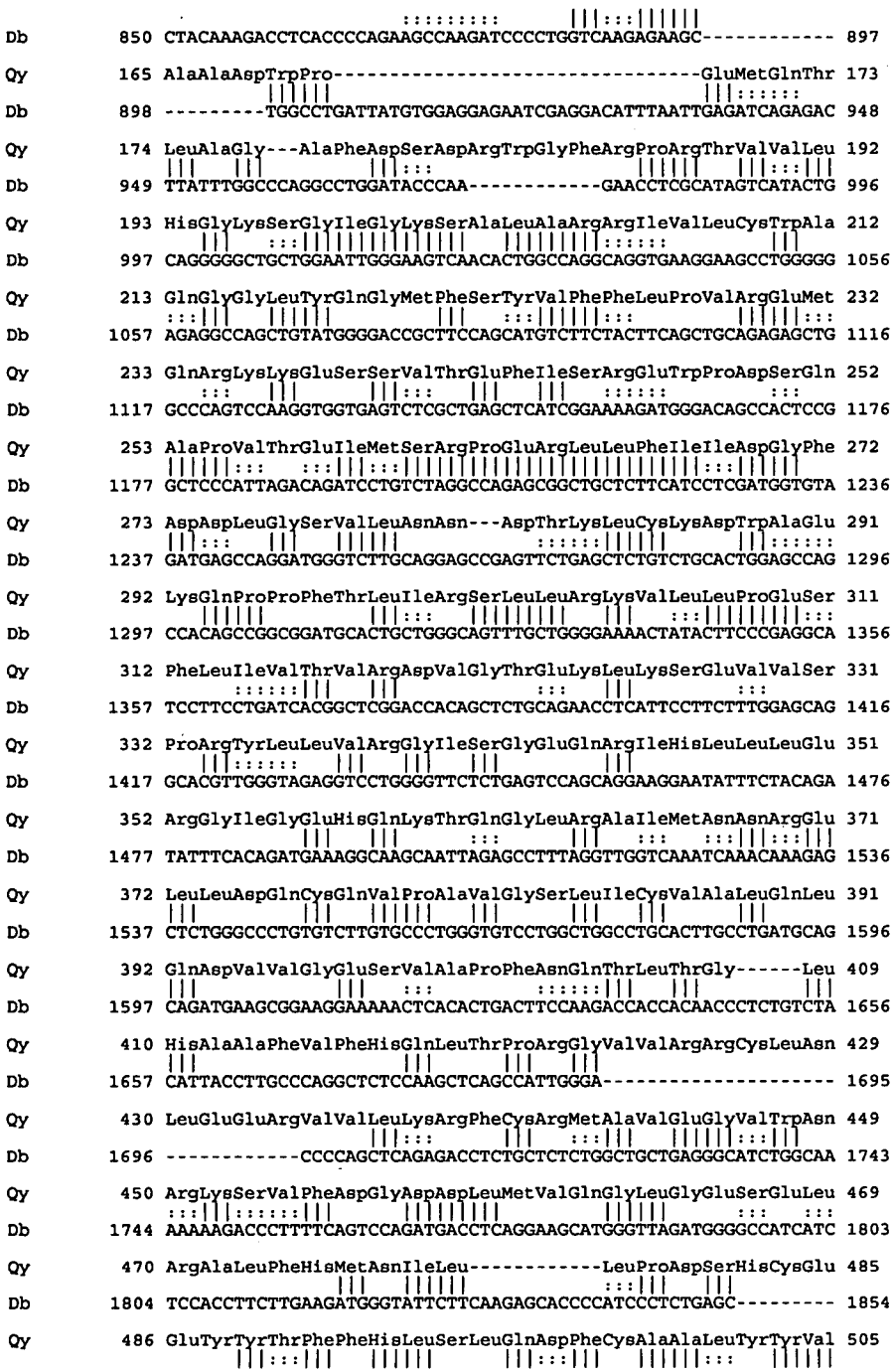


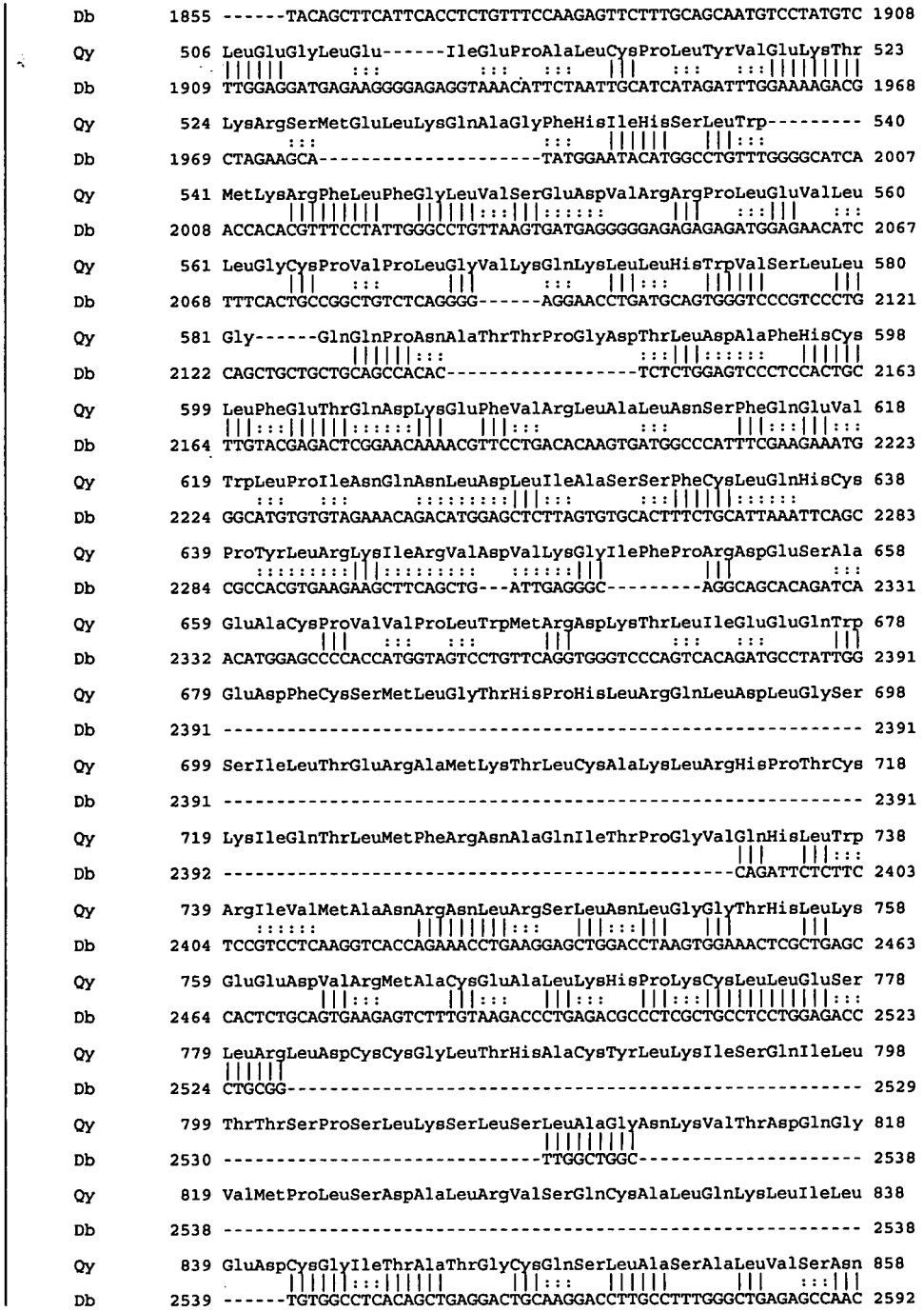
RESULT 2
US-09-388-221B-3
; Sequence 3, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:

```
;  APPLICANT: Reed, John C.
;  TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
;  FILE REFERENCE: P-LJ 3650
;  CURRENT APPLICATION NUMBER: US/09/388,221B
;  CURRENT FILING DATE:  1999-09-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 4200
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(4197)
US-09-388-221B-3

Alignment Scores:
Pred. No.:                1.83e-90      Length:          4200
Score:                    949.00        Matches:         387
Percent Similarity:       35.79%        Conservative:    190
Best Local Similarity:    24.01%        Mismatches:      458
Query Match:              13.42%        Indels:          579
DB:                       4             Gaps:            55

US-10-066-521-6 (1-1344) x US-09-388-221B-3 (1-4200)

Qy          11 SerTyrGlyLeuGlnTrpCysLeuTyrGlu---LeuAspLysGluGluPheGlnThrPhe 29
Db          13 GCCTGGGGCCGCCTGGCCTGTTACTTGGAGTTCCTGAAGAAGGAGGAGCTGAAGGAGTTC 72

Qy          30 LysGluLeuLeuLysLysLysSer---SerGluSerThrThrCysSerIleProGlnPhe 48
Db          73 CAGCTTCTGCTCGCCAATAAAGCGCACTCCAGGAGCTCTTCGGGTGAGACACCCGCTCAG 132

Qy          49 GluIleGluAsnAlaAsnValGluCysLeuAlaLeuLeuLeuHisGluTyrTyrGlyAla 68
Db         133 CCAGAGAAGACGAGTGGCATGGAGGTGGCCTCGTACCTGGTGGCTCAG---TATGGGGAG 189

Qy          69 SerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArgThrLeuSer 88
Db         190 CAGCGGGCCTGGGACCTAGCCCTCCATACCTGGGAGCAGATGGGGCTGAGGTCACTGTGC 249

Qy          89 GluLysAlaArgAspAsp---------------------------------------------- 94
Db         250 GCCCAAGCCCAGGAAGGGGCAGGCCACTCTCCCTCATTCCCCTACAGCCCAAGTGAACCC 309

Qy          94 ---------------------------------------------------------------- 94
Db         310 CACCTGGGGTCTCCCAGCCAACCCACCTCCACCGCAGTGCTAATGCCCTGGATCCATGAA 369

Qy          94 ---------------------------------------------------------------- 94
Db         370 TTGCCGGCGGGGTGCACCCAGGGCTCAGAGAGAAGGGTTTTGAGACAGCTGCCTGACACA 429

Qy          95 ------------MetLysLysIleSerGlnAlaMet---------------------- 102
Db         430 TCTGGACGCCGCTGGAGAGAAATCTCTGCCTCACTCCTCTACCAAGCTCTTCCAAGCTCC 489

Qy         102 ---------------------------------------------------------------- 102
Db         490 CCAGACCATGAGTCTCCAAGCCAGGAGTCACCCAACGCCCCCACATCCACAGCAGTGCTG 549

Qy         103 ----------------------------------------GluGlnGluGlyAla--- 107
Db         550 GGGAGCTGGGGATCCCCACCTCAGCCCAGCCTAGCACCCAGAGAGCAGGAGGCTCCTGGG 609

Qy         108 -------------------------------------ThrAlaAlaGluThrGluGlu 114
Db         610 ACCCAATGGCCTCTGGATGAAACGTCAGGAATTTACTACACAGAAATCAGAGAAAGAGAG 669

Qy         115 GlnGluIleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGln 134
Db         670 AGAGAGAAATCAGAGAAAGGCAGGCCCCCATGGGCAGCGGTGGTAGGAACGCCCCCACAG 729

Qy         135 GlyHisGlyGly---------------------------------------------- 138
Db         730 GCGCACACCAGCCTACAGCCCCACCACCACCCATGGGAGCCTTCTGTGAGAGAGAGCCTC 789

Qy         139 ---AspThrTrpAspTyrLysSerHisValMetThr---LysPhe--------------- 151
Db         790 TGTTCCACATGGCCCTGGAAAAATGAGGATTTTAACCAAAAATTCACACAGCTGCTACTT 849

Qy         152 --------------------AlaGluGluGluAspValArgArgSerPheGluAsnThr 164
Db         850 CTACAAAGACCTCACCCCAGAAGCCAAGATCCCCTGGTCAAGAGAAGC------------ 897

Qy         165 AlaAlaAspTrpPro---------------------------------GluMetGlnThr 173
Db         898 ---------TGGCCTGATTATGTGGAGGAGAATCGAGGACATTTAATTGAGATCAGAGAC 948

Qy         174 LeuAlaGly---AlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeu 192
Db         949 TTATTTGGCCCAGGCCTGGATACCCAA-----------GAACCTCGCATAGTCATACTG 996

Qy         193 HisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAla 212
Db         997 CAGGGGGCTGCTGGAATTGGGAAGTCAACACTGGCCAGGCAGGTGAAGGAAGCCTGGGGG 1056

Qy         213 GlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMet 232
Db        1057 AGAGGCCAGCTGTATGGGGACCGCTTCCAGCATGTCTTCTACTTCAGCTGCAGAGAGCTG 1116

Qy         233 GlnArgLysLysGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGln 252
Db        1117 GCCCAGTCCAAGGTGGTGAGTCTCGCTGAGCTCATCGGAAAAGATGGGACAGCCACTCCG 1176

Qy         253 AlaProValThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPhe 272
Db        1177 GCTCCCATTAGACAGATCCTGTCTAGGCCAGAGCGGCTGCTCTTCATCCTCGATGGTGTA 1236

Qy         273 AspAspLeuGlySerValLeuAsnAsn---AspThrLysLeuCysLysAspTrpAlaGlu 291
Db        1237 GATGAGCCAGGATGGGTCTTGCAGGAGCCGAGTTCTGAGCTCTGTCTGCACTGGAGCCAG 1296

Qy         292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSer 311
Db        1297 CCACAGCCGGCGGATGCACTGCTGGGCAGTTTGCTGGGGAAAACTATACTTCCCGAGGCA 1356

Qy         312 PheLeuIleValThrValArgAspValGlyThrGluLysLeuLysSerGluValValSer 331
Db        1357 TCCTTCCTGATCACGGCTCGGACCACAGCTCTGCAGAACCTCATTCCTTCTTTGGAGCAG 1416

Qy         332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGlu 351
Db        1417 GCACGTTGGGTAGAGGTCCTGGGGTTCTCTGAGTCCAGCAGGAAGGAATATTTCTACAGA 1476

Qy         352 ArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGlu 371
Db        1477 TATTTCACAGATGAAAGGCAAGCAATTAGAGCCTTTAGGTTGGTCAAATCAAACAAAGAG 1536

Qy         372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu 391
Db        1537 CTCTGGGCCCTGTGTCTTGTGCCCTGGGTGTCCTGGCTGGCCTGCACTTGCCTGATGCAG 1596

Qy         392 GlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeuThrGly------Leu 409
Db        1597 CAGATGAAGCGGAAGGAAAAACTCACACTGACTTCCAAGACCACCACAACCCTCTGTCTA 1656

Qy         410 HisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsn 429
Db        1657 CATTACCTTGCCCAGGCTCTCCAAGCTCAGCCATTGGGA---------------------- 1695

Qy         430 LeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsn 449
Db        1696 ------------CCCCAGCTCAGAGACCTCTGCTCTCTGGCTGCTGAGGGCATCTGGCAA 1743
```


Qy 450 ArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeu 469
Db 1744 AAAAAGACCCTTTTCAGTCCAGATGACCTCAGGAAGCATGGGTTAGATGGGGCCATCATC 1803
Qy 470 ArgAlaLeuPheHisMetAsnIleLeu----------LeuProAspSerHisCysGlu 485
Db 1804 TCCACCTTCTTGAAGATGGGTATTCTTCAAGAGCACCCCATCCCTCTGAGC--------- 1854
Qy 486 GluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrVal 505
Db 1855 ------TACAGCTTCATTCACCTCTGTTTCCAAGAGTTCTTTGCAGCAATGTCCTATGTC 1908
Qy 506 LeuGluGlyLeuGlu------IleGluProAlaLeuCysProLeuTyrValGluLysThr 523
Db 1909 TTGGAGGATGAGAAGGGGAGAGGTAAACATTCTAATTGCATCATAGATTTGGAAAAGACG 1968
Qy 524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp--------- 540
Db 1969 CTAGAAGCA----------TATGGAATACATGGCCTGTTTGGGGCATCA 2007
Qy 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560
Db 2008 ACCACACGTTTCCTATTGGGCCTGTTAAGTGATGAGGGGGAGAGAGAGATGGAGAACATC 2067
Qy 561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeu 580
Db 2068 TTTCACTGCCGGCTGTCTCAGGGG------AGGAACCTGATGCAGTGGGTCCCGTCCCTG 2121
Qy 581 Gly------GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCys 598
Db 2122 CAGCTGCTGCTGCAGCCACAC----------TCTCTGGAGTCCCTCCACTGC 2163
Qy 599 LeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618
Db 2164 TTGTACGAGACTCGGAACAAAACGTTCCTGACACAAGTGATGGCCCATTTCGAAGAAATG 2223
Qy 619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCys 638
Db 2224 GGCATGTGTGTAGAAACAGACATGGAGCTCTTAGTGTGCACTTTCTGCATTAAATTCAGC 2283
Qy 639 ProTyrLeuArgLysIleArgValAspValLysGlyIleProArgAspGluSerAla 658
Db 2284 CGCCACGTGAAGAAGCTTCAGCTG---ATTGAGGGC---------AGGCAGCACAGATCA 2331
Qy 659 GluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrp 678
Db 2332 ACATGGAGCCCCACCATGGTAGTCCTGTTCAGGTGGGTCCCAGTCACAGATGCCTATTGG 2391
Qy 679 GluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySer 698
Db 2391 ---------- 2391
Qy 699 SerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCys 718
Db 2391 ---------- 2391
Qy 719 LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrp 738
Db 2392 ----------CAGATTCTCTTC 2403
Qy 739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLys 758
Db 2404 TCCGTCCTCAAGGTCACCAGAAACCTGAAGGAGCTGGACCTAAGTGGAAACTCGCTGAGC 2463
Qy 759 GluGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSer 778
Db 2464 CACTCTGCAGTGAAGAGTCTTTGTAAGACCCTGAGACGCCCTCGCTGCCTCCTGGAGACC 2523
Qy 779 LeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeu 798
Db 2524 CTGCGG---------- 2529
Qy 799 ThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGly 818
Db 2530 ----------TTGGCTGGC---------- 2538
Qy 819 ValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeu 838
Db 2538 ---------- 2538
Qy 839 GluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsn 858
Db 2539 ------TGTGGCCTCACAGCTGAGGACTGCAAGGACCTTGCCTTTGGGCTGAGAGCCAAC 2592
Qy 859 ArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeu 878
Db 2593 CAGACC---------- 2598
Qy 879 LeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCys 898
Db 2598 ---------- 2598
Qy 899 HisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeu 918
Db 2599 ----------CTG 2601
Qy 919 ThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGlu 938
Db 2602 ACCGAGCTGGACCTGAGCTTCAATGTGCTCACGGATGCTGGAGCCAAACACCTTTGCCAG 2661
Qy 939 ValMetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThr 958
Db 2662 AGACTGAGACAGCCGAGCTGCAAGCTACAGCGACTGCAGCTGGTCAGCTGTGGCCTCACG 2721
Qy 959 AlaAlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeu 978
Db 2722 TCTGACTGCTGCCAGGACCTGGCCTCTGTGCTTAGTGCCAGCCCCAGCCTGAAGGAGCTA 2781
Qy 979 AspLeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLys 998
Db 2782 GACCTGCAGCAGAACAACCTGGATGACGTTGGCGTGCGACTGCTCTGTGAGGGGCTCAGG 2841
Qy 999 GlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCys----------Gly 1013
Db 2842 CATCCTGCCTGCAAACTCATACGCCTGGGGAAACCAAGTGTGATGACCCCTACTGAGGGC 2901
Qy 1014 LeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArg--------- 1030
Db 2902 CTG------GATACGGGAGAGATGAGTAATAGCACATCCTCACTCAAGCGGCAGAGACTC 2955
Qy 1031 ----------HisLeuThrSerLeuAsnLeu---------- 1037
Db 2956 GGATCAGAGAGGGCGGCTTCCCATGTTGCTCAGGCTAATCTCAAACTCCTGGACGTGAGC 3015
Qy 1038 ----------ValGlnAsnAsnPheSerProLysGlyMet---MetLys 1049
Db 3016 AAGATCTTCCCAATTGCTGAGATTGCAGAGGAAAGCTCCCCAGAGGTAGTACCGGTGGAA 3075
Qy 1050 Leu-CysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTr 1069
Db 3076 CTCTTGTGCGTGCCTTCTCCTGCCTCTCAAGGGGACCTGCATACGAAGCCTTTGG----- 3130
Qy 1069 pGlnTyrProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuLysProArgVa 1089
Db 3130 ---------- 3130
Qy 1089 lValIleAspGlySerTrpHisSerPheAspGluAspAspArgHisLysIleGlyLeuTh 1109
Db 3131 ----------GGACTGAC 3138
Qy 1109 rPheArgLeuProGluSerArgAlaTrpProCysAlaLeuLeuTrpGlyMetAsnProGl 1129
Db 3139 GATGACTTCTGGGGCCCCACGGGGC----------CTGTGGCTACTGAGGTAGTT 3183
Qy 1129 uGlnLysLysArgValSerLeuLeuAlaGlyAspPheLysSerSerThrArgPheAlaLy 1149

```
Db       3184 GACAAAGAAAAGA--------------------------ACTTGTACCGAGTTCACT-- 3214

Qy       1149 sSerLeuCysLeuAlaThrAlaAsnGlyGluSerGlnArgValAspAsnVal-GluGlnS 1169

Db       3215 -TCCCTGTAGCTGGCTCCTACCGCTGGCCCAACA---CGGGTCTCTGCTTTGTGATGAGA 3270

Qy       1169 erSerProGlnProMetAlaGlyThrGluHisLysGlnAspLysMetLeuSerValGly- 1188

Db       3271 GAAGCGGTGAC--------------------CGTTGAGATTGAATTCTGTGTGTGGGAC 3309

Qy       1189 --TyrSerGlyAlaTrpSerGluThrAlaGluLeuGluGlyLeuGlySerAsnSerAlaA 1208

Db       3310 CAGTTCCTGGGTGAGATCAACCCACAGCACAGCTGGATGGT---GGCAGGGCCTCTGCTG 3366

Qy       1208 spHisAspHisGlyGlyMetAlaTrpSerLeuGlyArgGluLeuSerSerArgGlyLeuC 1228

Db       3367 GACATCAA------GGCTGAGCCTGGAGCTGTGGA---AGCTGTGCACCTCCCTCACTTT 3417

Qy       1228 ys------ProThrValLeuMetThrThrAlaValCysProGlyHisTrpGluArgLeuG 1246

Db       3418 GTGGCTCTCCAAGGGG-GCCATGTGGACACATCCCTGT---TCCAAATGGCCCACTTTAA 3473

Qy       1246 lySerArgGly------------------------------------------------- 1249

Db       3474 AGAGGAGGGGATGCTCCTGGAGAAGCCAGCCAGGGTGGAGCTGCATCACATAGTTCTGGA 3533

Qy       1249 ------------------------------------------------------------ 1249

Db       3534 AAACCCCAGCTTCTCCCCCTTGGGAGTCCTCCTGAAAATGATCCATAATGCCCTGCGCTT 3593

Qy       1250 -----------------TrpCys--------------------LeuAsnSerAlaAspA 1257

Db       3594 CATTCCCGTCACCTCTGTGGTGTTGCTTTACCACCGCGTCCATCCTGAGGAAGTCACCTT 3653

Qy       1257 spHisSer--------------------------GlyValSerTrpSerLeuGlyAlaA 1268

Db       3654 CCACCTCTACCTGATCCCAAGTGACTGCTCCATTCGGAAGGAACTGGAGC---------T 3704

Qy       1268 laGlyLeuGluGlyLeuValSerAsnSerAlaAspAspHisSerGlyValAla---TrpS 1287

Db       3705 CTGCTATCGAAGCCCTGGAGAAGACCAGCTGTTCTCGGAGTTCTACGTTGGCCACTTGGG 3764

Qy       1287 erLeuGlyAla-Ala----------------------------GlyLeuGluGlyLeu 1296

Db       3765 ATCAGGGATCAGGCTGCAAGTGAAAGACAAGAAAGATGAGACTCTGGTGTGGGAGGCCTT 3824

Qy       1297 ----------------------------ValSerAsnSerAlaAspAspHisSerGly 1306

Db       3825 GGTGAAACCAGGAGATCTCATGCCTGCAACTACTCTGATCCCTCCAGCCCGCATAGCCGT 3884

Qy       1307 ------ValSerTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuValSerAsnSerAla 1324

Db       3885 ACCTTCACCTCTGGATGCCCCGCAGTTGCTGCACTTTGTGGACCAGTATCGAGAGCAGCT 3944

Qy       1325 AspAspHisSerGlyValSerTrpSerLeu 1334

Db       3945 GATAGCCCGAGTGACATCGG-TGGAGGTTG 3973

RESULT 3
US-09-388-221B-5
; Sequence 5, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
;  APPLICANT: Reed, John C.
;  TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
;  FILE REFERENCE: P-LJ 3650
;  CURRENT APPLICATION NUMBER: US/09/388,221B
;  CURRENT FILING DATE:  1999-09-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 4332
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(4332)
US-09-388-221B-5

Alignment Scores:
Pred. No.:                1.94e-90        Length:          4332
Score:                    949.00          Matches:         359
Percent Similarity:       36.80%          Conservative:    179
Best Local Similarity:    24.56%          Mismatches:      423
Query Match:              13.42%          Indels:          502
DB:                       4               Gaps:            49

US-10-066-521-6 (1-1344) x US-09-388-221B-5 (1-4332)

Qy         11 SerTyrGlyLeuGlnTrpCysLeuTyrGlu---LeuAspLysGluGluPheGlnThrPhe 29

Db         13 GCCTGGGGCCGCCTGGCCTGTTACTTGGAGTTCCTGAAGAAGGAGGAGCTGAAGGAGTTC 72

Qy         30 LysGluLeuLeuLysLysLysSer---SerGluSerThrThrCysSerIleProGlnPhe 48

Db         73 CAGCTTCTGCTCGCCAATAAAGCGCACTCCAGGAGCTCTTCGGGTGAGACACCCGCTCAG 132

Qy         49 GluIleGluAsnAlaAsnValGluCysLeuAlaLeuLeuLeuHisGluTyrTyrGlyAla 68

Db        133 CCAGAGAAGACGAGTGGCATGGAGGTGGCCTCGTACCTGGTGGCTCAG---TATGGGGAG 189

Qy         69 SerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArgThrLeuSer 88

Db        190 CAGCGGGCCTGGGACCTAGCCCTCCATACCTGGGAGCAGATGGGGCTGAGGTCACTGTGC 249

Qy         89 GluLysAlaArgAspAsp------------------------------------------ 94

Db        250 GCCCAAGCCCAGGAAGGGGCAGGCCACTCTCCCTCATTCCCCTACAGCCCAAGTGAACCC 309

Qy         94 ------------------------------------------------------------ 94

Db        310 CACCTGGGGTCTCCCAGCCAACCCACCTCCACCGCAGTGCTAATGCCCTGGATCCATGAA 369

Qy         94 ------------------------------------------------------------ 94

Db        370 TTGCCGGCGGGGTGCACCCAGGGCTCAGAGAGAAGGGTTTTGAGACAGCTGCCTGACACA 429

Qy         95 ------------MetLysLysIleSerGlnAlaMet----------------------- 102

Db        430 TCTGGACGCCGCTGGAGAGAAATCTCTGCCTCACTCCTCTACCAAGCTCTTCCAAGCTCC 489

Qy        102 ------------------------------------------------------------ 102

Db        490 CCAGACCATGAGTCTCCAAGCCAGGAGTCACCCAACGCCCCCACATCCACAGCAGTGCTG 549

Qy        103 ----------------------------------------GluGlnGluGlyAla--- 107

Db        550 GGGAGCTGGGGATCCCCACCTCAGCCCAGCCTAGCACCCAGAGAGCAGGAGGCTCCTGGG 609

Qy        108 -----------------------------------ThrAlaAlaGluThrGluGlu 114

Db        610 ACCCAATGGCCTCTGGATGAAACGTCAGGAATTTACTACACAGAAATCAGAGAAAGAGAG 669

Qy        115 GlnGluIleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGln 134

Db        670 AGAGAGAAATCAGAGAAAGGCAGGCCCCCATGGGCAGCGGTGGTAGGAACGCCCCCACAG 729

Qy        135 GlyHisGlyGly------------------------------------------------ 138

Db        730 GCGCACACCAGCCTACAGCCCCACCACCACCCATGGGAGCCTTCTGTGAGAGAGAGCCTC 789

Qy        139 ---AspThrTrpAspTyrLysSerHisValMetThr---LysPhe--------------- 151

Db        790 TGTTCCACATGGCCCTGGAAAAATGAGGATTTTAACCAAAAATTCACACAGCTGCTACTT 849

Qy        152 --------------------AlaGluGluGluAspValArgArgSerPheGluAsnThr 164
```


Db 850 CTACAAAGACCTCACCCCAGAAGCCAAGATCCCCTGGTCAAGAGAAGC 897
Qy 165 AlaAlaAspTrpPro-----GluMetGlnThr 173
Db 898 ---------TGGCCTGATTATGTGGAGGAGAATCGAGGACATTTAATTGAGATCAGAGAC 948
Qy 174 LeuAlaGly---AlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeu 192
Db 949 TTATTTGGCCCAGGCCTGGATACCCAA-----------GAACCTCGCATAGTCATACTG 996
Qy 193 HisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAla 212
Db 997 CAGGGGGCTGCTGGAATTGGGAAGTCAACACTGGCCAGGCAGGTGAAGGAAGCCTGGGGG 1056
Qy 213 GlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMet 232
Db 1057 AGAGGCCAGCTGTATGGGGACCGCTTCCAGCATGTCTTCTACTTCAGCTGCAGAGAGCTG 1116
Qy 233 GlnArgLysLysGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGln 252
Db 1117 GCCCAGTCCAAGGTGGTGAGTCTCGCTGAGCTCATCGGAAAAGATGGGACAGCCACTCCG 1176
Qy 253 AlaProValThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPhe 272
Db 1177 GCTCCCATTAGACAGATCCTGTCTAGGCCAGAGCGGCTGCTCTTCATCCTCGATGGTGTA 1236
Qy 273 AspAspLeuGlySerValLeuAsnAsn---AspThrLysLeuCysLysAspTrpAlaGlu 291
Db 1237 GATGAGCCAGGATGGGTCTTGCAGGAGCCGAGTTCTGAGCTCTGTCTGCACTGGAGCCAG 1296
Qy 292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSer 311
Db 1297 CCACAGCCGGCGGATGCACTGCTGGGCAGTTGCTGGGGAAAACTATACTTCCCGAGGCA 1356
Qy 312 PheLeuIleValThrValArgAspValGlyThrGluLysLeuLysSerGluValValSer 331
Db 1357 TCCTTCCTGATCACGGCTCGGACCACAGCTCTGCAGAACCTCATTCCTTCTTTGGAGCAG 1416
Qy 332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuGluGlu 351
Db 1417 GCACGTTGGGTAGAGGTCCTGGGGTTCTCTGAGTCCAGCAGGAAGGAATATTTCTACAGA 1476
Qy 352 ArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGlu 371
Db 1477 TATTTCACAGATGAAAGGCAAGCAATTAGAGCCTTTAGGTTGGTCAAATCAAACAAAGAG 1536
Qy 372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu 391
Db 1537 CTCTGGGCCCTGTGTCTTGTGCCCTGGGTGTCCTGGCTGGCCTGCACTTGCCTGATGCAG 1596
Qy 392 GlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeuThrGly------Leu 409
Db 1597 CAGATGAAGCGGAAGGAAAAACTCACACTGACTTCCAAGACCACCACAACCCTCTGTCTA 1656
Qy 410 HisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsn 429
Db 1657 CATTACCTTGCCCAGGCTCTCCAAGCTCAGCCATTGGGA---------- 1695
Qy 430 LeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsn 449
Db 1696 -----------CCCCAGCTCAGAGACCTCTGCTCTCTGGCTGCTGAGGGCATCTGGCAA 1743
Qy 450 ArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeu 469
Db 1744 AAAAAGACCCTTTTCAGTCCAGATGACCTCAGGAAGCATGGGTTAGATGGGGCCATCATC 1803
Qy 470 ArgAlaLeuPheHisMetAsnIleLeu-----------LeuProAspSerHisCysGlu 485
Db 1804 TCCACCTTCTTGAAGATGGGTATTCTTCAAGAGCACCCCATCCCTCTGAGC--------- 1854
Qy 486 GluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrVal 505


Db 1855 ------TACAGCTTCATTCACCTCTGTTTCCAAGAGTTCTTTGCAGCAATGTCCTATGTC 1908
Qy 506 LeuGluGlyLeuGlu------IleGluProAlaLeuCysProLeuTyrValGluLysThr 523
Db 1909 TTGGAGGATGAGAAGGGGAGAGGTAAACATTCTAATTGCATCATAGATTTGGAAAAGACG 1968
Qy 524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp--------- 540
Db 1969 CTAGAAGCA--------------------TATGGAATACATGGCCTGTTTGGGGCATCA 2007
Qy 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560
Db 2008 ACCACACGTTTCCTATTGGGCCTGTTAAGTGATGAGGGGGAGAGAGAGATGGAGAACATC 2067
Qy 561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeu 580
Db 2068 TTTCACTGCCGGCTGTCTCAGGGG------AGGAACCTGATGCAGTGGGTCCCGTCCCTG 2121
Qy 581 Gly------GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCys 598
Db 2122 CAGCTGCTGCTGCAGCCACAC----------------TCTCTGGAGTCCCTCCACTGC 2163
Qy 599 LeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618
Db 2164 TTGTACGAGACTCGGAACAAAACGTTCCTGACACAAGTGATGGCCCATTTCGAAGAAATG 2223
Qy 619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCys 638
Db 2224 GGCATGTGTGTAGAAACAGACATGGAGCTCTTAGTGTGCACTTTCTGCATTAAATTCAGC 2283
Qy 639 ProTyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerAla 658
Db 2284 CGCCACGTGAAGAAGCTTCAGCTG---ATTGAGGGC---------AGGCAGCACAGATCA 2331
Qy 659 GluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrp 678
Db 2332 ACATGGAGCCCCACCATGGTAGTCCTGTTCAGGTGGGTCCCAGTCACAGATGCCTATTGG 2391
Qy 679 GluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySer 698
Db 2391 ---------- 2391
Qy 699 SerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCys 718
Db 2391 ---------- 2391
Qy 719 LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrp 738
Db 2392 ----------CAGATTCTCTTC 2403
Qy 739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLys 758
Db 2404 TCCGTCCTCAAGGTCACCAGAAACCTGAAGGAGCTGGACCTAAGTGGAAACTCGCTGAGC 2463
Qy 759 GluGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSer 778
Db 2464 CACTCTGCAGTGAAGAGTCTTTGTAAGACCCTGAGACGCCCTCGCTGCCTCCTGGAGACC 2523
Qy 779 LeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeu 798
Db 2524 CTGCGG---------- 2529
Qy 799 ThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGly 818
Db 2530 ----------TTGGCTGGC---------- 2538
Qy 819 ValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeu 838
Db 2538 ---------- 2538
Qy 839 GluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsn 858
Db 2539 ------TGTGGCCTCACAGCTGAGGACTGCAAGGACCTTGCCTTTGGGCTGAGAGCCAAC 2592

```
Qy        859 ArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeu 878
              ::::::
Db       2593 CAGACC------------------------------------------------------ 2598

Qy        879 LeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCys 898

Db       2598 ------------------------------------------------------------ 2598

Qy        899 HisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeu 918
                                                                        |||
Db       2599 ----------------------------------------------------------CTG 2601

Qy        919 ThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGlu 938
              |||   |||   ||||||   |||   :::   |||   |||   |||   ||||||:::
Db       2602 ACCGAGCTGGACCTGAGCTTCAATGTGCTCACGGATGCTGGAGCCAAACACCTTTGCCAG 2661

Qy        939 ValMetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThr 958
                 :::|||:::|||||||||   ||||||   |||:::||||||   |||   ||||||
Db       2662 AGACTGAGACAGCCGAGCTGCAAGCTACAGCGACTGCAGCTGGTCAGCTGTGGCCTCACG 2721

Qy        959 AlaAlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeu 978
              :::   ||||||:::   |||:::   |||:::|||   |||      ||||||   |||
Db       2722 TCTGACTGCTGCCAGGACCTGGCCTCTGTGCTTAGTGCCAGCCCCAGCCTGAAGGAGCTA 2781

Qy        979 AspLeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLys 998
              ||||||      |||   |||   |||   ||||||      ||||||||||||||:::
Db       2782 GACCTGCAGCAGAACAACCTGGATGACGTTGGCGTGCGACTGCTCTGTGAGGGGCTCAGG 2841

Qy        999 GlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCys--------------Gly 1013
                          |||   ||||||||   :::                        |||
Db       2842 CATCCTGCCTGCAAACTCATACGCCTGGGGAAACCAAGTGTGATGACCCCTACTGAGGGC 2901

Qy       1014 LeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArg--------- 1030
              |||      |||      |||      :::      |||      |||
Db       2902 CTG------GATACGGGAGAGATGAGTAATAGCACATCCTCACTCAAGCGGCAGAGACTC 2955

Qy       1031 --------------------HisLeuThrSerLeuAsnLeu------------------ 1037
                                  |||:::      ||||||
Db       2956 GGATCAGAGAGGGCGGCTTCCCATGTTGCTCAGGCTAATCTCAAACTCCTGGACGTGAGC 3015

Qy       1038 --------------------ValGlnAsnAsnPheSerProLysGlyMet---MetLys 1049
                                  :::            ||||||:::   :::   ::::::
Db       3016 AAGATCTTCCCAATTGCTGAGATTGCAGAGGAAAGCTCCCCAGAGGTAGTACCGGTGGAA 3075

Qy       1050 Leu-CysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTr 1069
              ||| |||:::      |||      |||      ||||||
Db       3076 CTCTTGTGCGTGCCTTCTCCTGCCTCTCAAGGGGACCTGCATACGAAGCCTTTGG----- 3130

Qy       1069 pGlnTyrProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuLysProArgVa 1089

Db       3130 ------------------------------------------------------------ 3130

Qy       1089 lValIleAspGlySerTrpHisSerPheAspGluAspAspArgHisLysIleGlyLeuTh 1109
                                                                    ||||||||
Db       3131 ----------------------------------------------------GGACTGAC 3138

Qy       1109 rPheArgLeuProGluSerArgAlaTrpProCysAlaLeuLeuTrpGlyMetAsnProGl 1129
              |      |||            ||||||   :::
Db       3139 GATGACTTCTGGGGCCCCACGGGGC--------------CTGTGGCTACTGAGGTAGTT 3183

Qy       1129 uGlnLysLysArgValSerLeuLeuAlaGlyAspPheLysSerSerThrArgPheAlaLy 1149
                 |||||||||                        :::   |||   |||
Db       3184 GACAAAGAAAAGA-------------------------ACTTGTACCGAGTTCACT-- 3214

Qy       1149 sSerLeuCysLeuAlaThrAlaAsnGlyGluSerGlnArgValAspAsnVal-GluGlnS 1169
               ||||||   ||||||         |||   :::   ||||||      ::: ::::::
Db       3215 -TCCCTGTAGCTGGCTCCTACCGCTGGCCCAACA---CGGGTCTCTGCTTTGTGATGAGA 3270

Qy       1169 erSerProGlnProMetAlaGlyThrGluHisLysGlnAspLysMetLeuSerValGly- 1188
               |||                              :::   |||   :::|||   ||||||
Db       3271 GAAGCGGTGAC--------------------CGTTGAGATTGAATTCTGTGTGTGGGAC 3309
```

```
Qy       1189 --TyrSerGlyAlaTrpSerGluThrAlaGluLeuGluGlyLeuGlySerAsnSerAlaA 1208
                 |||            ||||||:::|||:::|||   |||      ||||||
Db       3310 CAGTTCCTGGGTGAGATCAACCCACAGCACAGCTGGATGGT---GGCAGGGCCTCTGCTG 3366

Qy       1208 spHisAspHisGlyGlyMetAlaTrpSerLeuGlyArgGluLeuSerSerArgGlyLeuC 1228
                |||      |||   |||||||||   |||         :::         ||||
Db       3367 GACATCAA------GGCTGAGCCTGGAGCTGTGGA---AGCTGTGCACCTCCCTCACTTT 3417

Qy       1228 ys------ProThrValLeuMetThrThrAlaValCysProGlyHisTrpGluArgLeuG 1246
              ||      |||         |||   |||      |||      |||      |||
Db       3418 GTGGCTCTCCAAGGGG-GCCATGTGGACACATCCCTGT---TCCAAATGGCCCACTTTAA 3473

Qy       1246 lySerArgGly------TrpCysLeuAsnSerAlaAspAspHisSerGlyValSerTrpS 1264
                 ||||||      |||                     |||         ||||
Db       3474 AGAGGAGGGGATGCTCCTGG--------------------AGAAGCCAGCCAGGGTGGA 3512

Qy       1264 er 1264
              ||
Db       3513 GC 3514
```

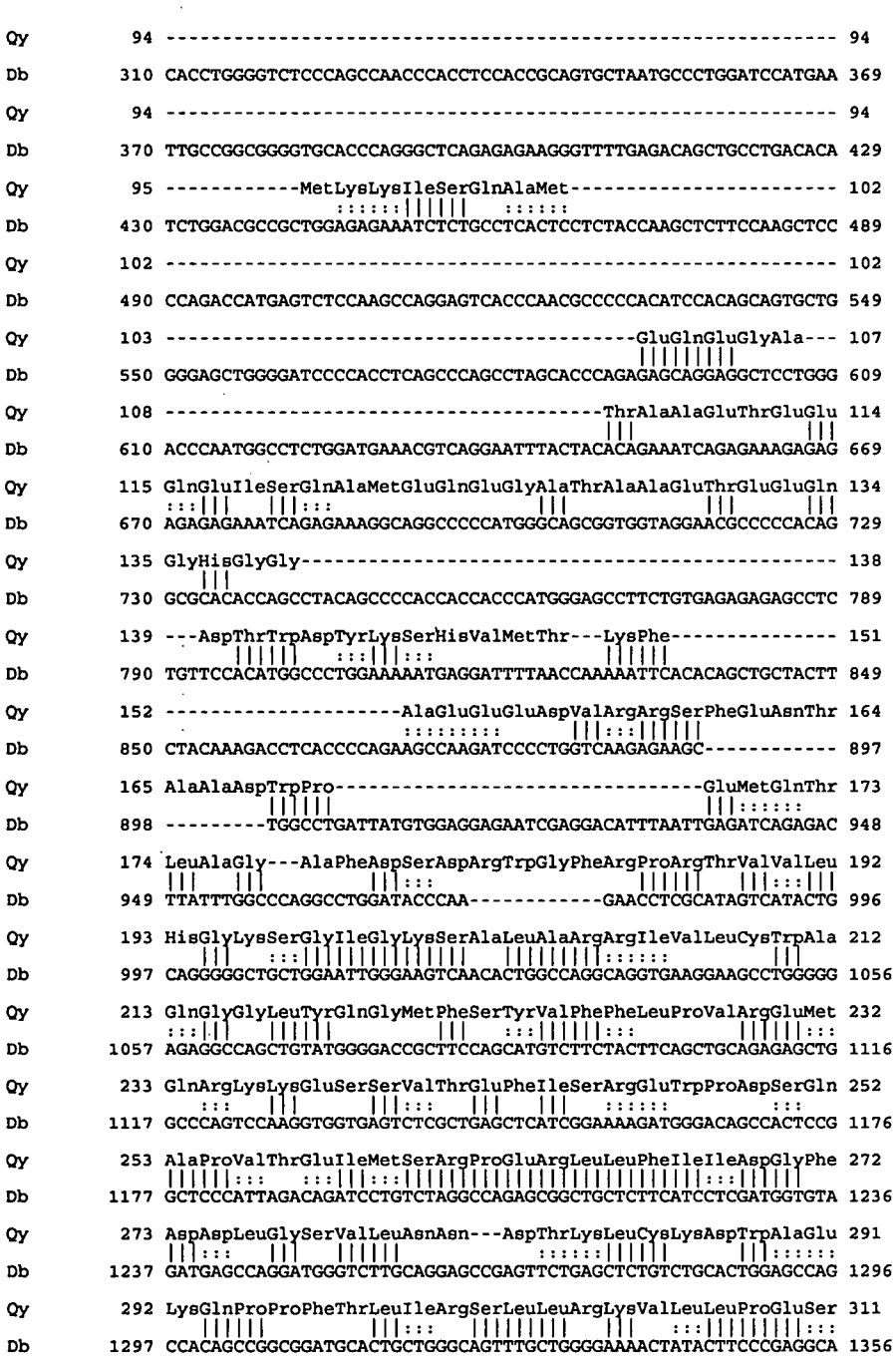
RESULT 4
US-09-388-221B-11
; Sequence 11, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 4466
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4272)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
US-09-388-221B-11

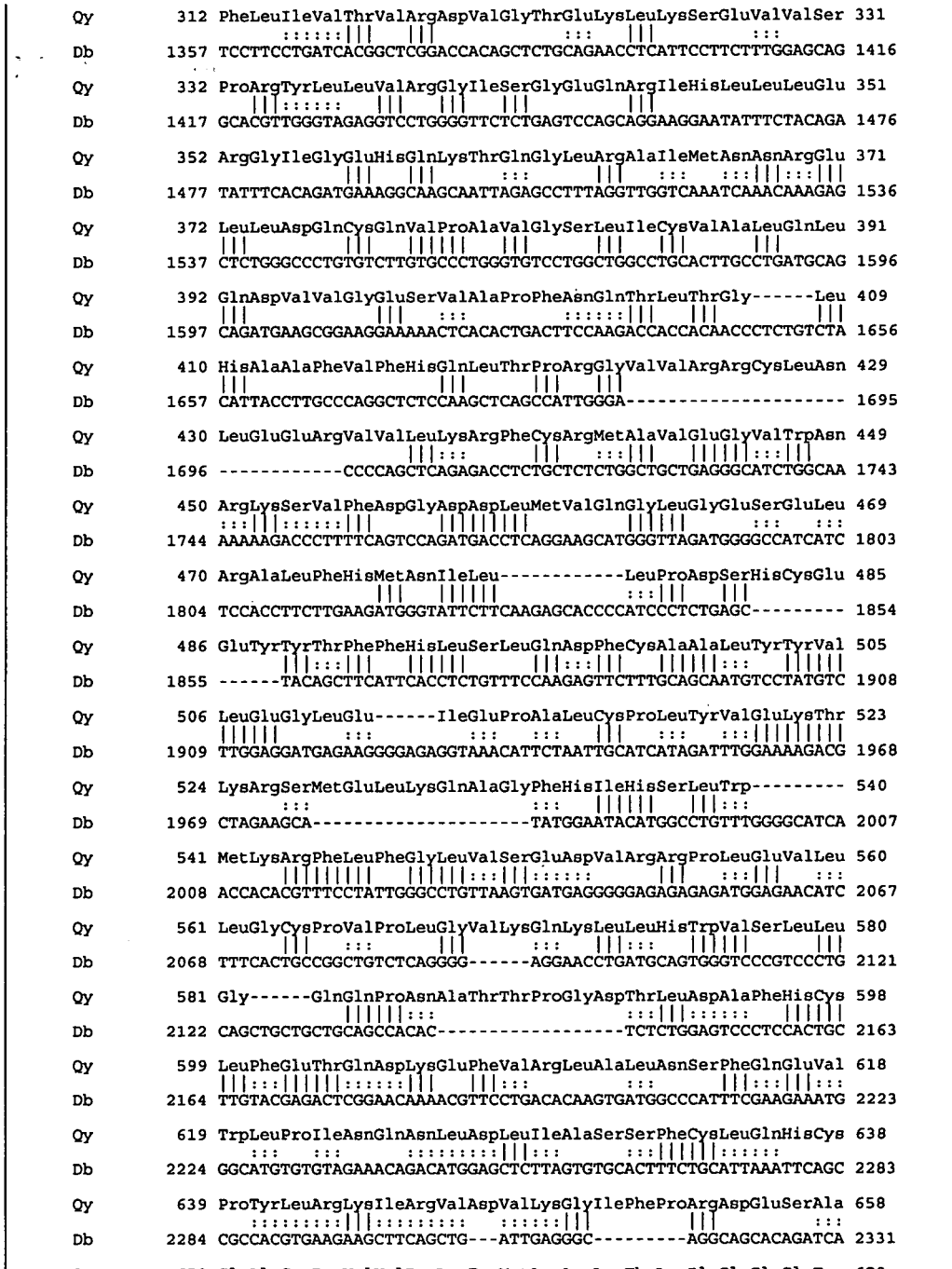
Alignment Scores:

Pred. No.:	2.64e-90	Length:	4466
Score:	948.00	Matches:	360
Percent Similarity:	38.47%	Conservative:	207
Best Local Similarity:	24.42%	Mismatches:	529
Query Match:	13.40%	Indels:	380
DB:	4	Gaps:	46

US-10-066-521-6 (1-1344) x US-09-388-221B-11 (1-4466)

```
Qy         11 SerTyrGlyLeuGlnTrpCysLeuTyrGlu---LeuAspLysGluGluPheGlnThrPhe 29
              ::::::|||         |||   |||   |||||||||   :::   |||
Db         13 GCCTGGGGCCGCCTGGCCTGTTACTTGGAGTTCCTGAAGAAGGAGGAGCTGAAGGAGTTC 72

Qy         30 LysGluLeuLeuLysLysLysSer---SerGluSerThrThrCysSerIleProGlnPhe 48
              :::   ||||||      |||:::   |||   |||::::::          |||
Db         73 CAGCTTCTGCTCGCCAATAAAGCGCACTCCAGGAGCTCTTCGGGTGAGACACCCGCTCAG 132

Qy         49 GluIleGluAsnAlaAsnValGluCysLeuAlaLeuLeuLeuHisGluTyrTyrGlyAla 68
                  :::   :::   :::|||      :::   |||:::   :::   ||||||
Db        133 CCAGAGAAGACGAGTGGCATGGAGGTGGCCTCGTACCTGGTGGCTCAG---TATGGGGAG 189

Qy         69 SerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArgThrLeuSer 88
                    ||||||      ::::::      :::|||   |||   ||||||:::|||
Db        190 CAGCGGGCCTGGGACCTAGCCCTCCATACCTGGGAGCAGATGGGGCTGAGGTCACTGTGC 249

Qy         89 GluLysAlaArgAspAsp------------------------------------------ 94
                 :::|||::::::
Db        250 GCCCAAGCCCAGGAAGGGGCAGGCCACTCTCCCTCATTCCCCTACAGCCCAAGTGAACCC 309
```



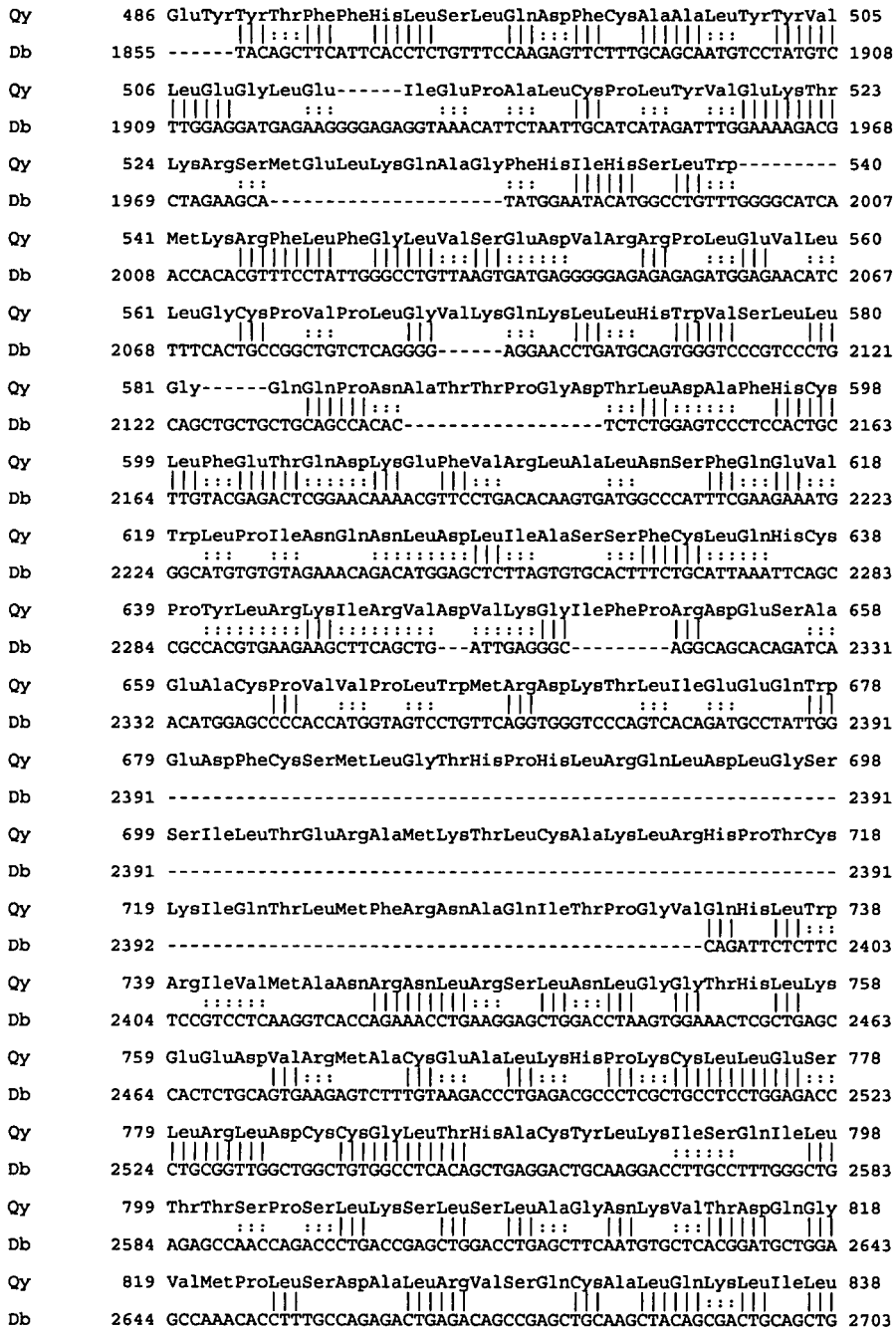


```
Db       2332 ACATGGAGCCCCACCATGGTAGTCCTGTTCAGGTGGGTCCCAGTCACAGATGCCTATTGG 2391

Qy        679 GluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySer 698

Db       2391 ------------------------------------------------------------ 2391

Qy        699 SerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCys 718

Db       2391 ------------------------------------------------------------ 2391

Qy        719 LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrp 738

Db       2392 ---------------------------------------------CAGATTCTCTTC 2403

Qy        739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLys 758

Db       2404 TCCGTCCTCAAGGTCACCAGAAACCTGAAGGAGCTGGACCTAAGTGGAAACTCGCTGAGC 2463

Qy        759 GluGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSer 778

Db       2464 CACTCTGCAGTGAAGAGTCTTTGTAAGACCCTGAGACGCCCTCGCTGCCTCCTGGAGACC 2523

Qy        779 LeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeu 798

Db       2524 CTGCGGTTGGCTGGCTGTGGCCTCACAGCTGAGGACTGCAAGGACCTTGCCTTTGGGCTG 2583

Qy        799 ThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGly 818

Db       2584 AGAGCCAACCAGACCCTGACCGAGCTGGACCTGAGCTTCAATGTGCTCACGGATGCTGGA 2643

Qy        819 ValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeu 838

Db       2644 GCCAAACACCTTTGCCAGAGACTGAGACAGCCGAGCTGCAAGCTACAGCGACTGCAGCTG 2703

Qy        839 GluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsn 858

Db       2704 GTCAGCTGTGGCCTCACGTCTGACTGCTGCCAGGACCTGGCCTCTGTGCTTAGTGCCAGC 2763

Qy        859 ArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeu 878

Db       2764 CCCAGCCTGAAGGAGCTAGACCTGCAGCAGAACAACCTGGATGACGTTGGCGTGCGACTG 2823

Qy        879 LeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCys 898

Db       2824 CTCTGTGAGGGGCTCAGGCATCCTGCCTGCAAACTCATACGCCTGGGGAAACCAAGTGTG 2883

Qy        899 HisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrp--- 917

Db       2884 ATGACCCCTACTGAGGGC---------CTGGATACGGGAGAGATGAGTAATAGCACATCC 2934

Qy        918 ---LeuThrHisLeuSerLeu-----------SerMetAsnProValGluAspAsnGly 932

Db       2935 TCACTCAAGCGGCAGAGACTCGGATCAGAGAGGGCGGCTTCCCATGTTGCTCAGGCTAAT 2994

Qy        933 ValLysLeuLeu----------------------CysGluValMetArgGluProSer 944

Db       2995 CTCAAACTCCTGGACGTGAGCAAGATCTTCCCAATTGCTGAGATTGCAGAGGAAAGCTCC 3054

Qy        945 CysHisLeuGlnAspLeuGluLeuVal-LysCys---------HisLeuThrAlaAlaCy 961

Db       3055 CCAGAGGTAGTACCGGTGGAACTCTTGTGCGTGCCTTCTCCTGCCTCTCAAGGGGACCTG 3114

Qy        961 sCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAspLeu-- 980

Db       3115 CATACGAAGCCTTTGGGGACTGACGATGACTTTCTGGGGCCTGAAGGAAATGTGGATGTT 3174

Qy        981 ----------------------ThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLe 993

Db       3175 GAGTTGATTGATAAGAGCACAAACAGATACAGCGTTTGGTTCCCCACTGCTGGCTGGTAT 3234

Qy        993 uCysGlu---------------------------GlyLeuLysGlnLysAsnSerValLe 1004

Db       3235 CTGTGGTCAGCCACAGGCCTCGGCTTCCTGGTAAGGGATGAGGTCACAGTGACGATTGCG 3294

Qy       1004 uThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLe 1024

Db       3295 TTTGGTTCCTGGAGTCAGCACCTGGCCCTGGACCTGCAGCACCATGAACAGTGGCTGGTG 3354

Qy       1024 uAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerPr 1044

Db       3355 GGCGGCCCCTTGTTTGATGTCACTGCAGAGC------------CAGAGGAGGCTGTCGCC 3402

Qy       1044 oLysGlyMetMetLysLeuCysSer------------AlaPheAlaCysProThrSerAs 1060

Db       3403 GAAATCCACCTCCCCCACTTCATCTCCCTCCAAGGTGAGGTGGACGTCTCCTGGTTTCTC 3462

Qy       1060 nLeuGlnIleIleGlyLeu------TrpLysTrpGlnTyrProValGlnIleArgLysLe 1078

Db       3463 GTTGCCCATTTTAAGAATGAAGGGATGGTCCTGGAG-CATCCAGCCCGGGTGGAGCCTTT 3521

Qy       1078 uLeuGluGluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHisSerPh 1098

Db       3522 CTATGCTGTCCTGGAA------AGCCCCAGCTTCTCTCTGATGGGCATCCTGCTGCGGAT 3575

Qy       1098 eAspGluAspAspArgHisLysIleGlyLeuThrPheArgLeuProGluSerArgAlaTr 1118

Db       3576 CGCCAGTGGGACTCGCCTCTCCATCCCCATCACTTCCAAC------------------- 3615

Qy       1118 pProCysAlaLeuLeuTrpGlyMetAsnProGluGln---LysLysArgValSerLeuLe 1137

Db       3616 ----ACATTGATCTATTATCACCCCCACCCCGAAGATATTAAGTTCCACTTGTACCTTGT 3671

Qy       1137 uAlaGlyAspPheLysSerSerThrArgPheAlaLysSerLeuCysLeuAlaThrAlaAs 1157

Db       3672 CCCCAGCGAC--------------------------GCCTTGCTAACAAAGGCGATAGA 3704

Qy       1157 nGlyGluSerGlnArgValAspAsnValGluGlnSerSerProGlnProMetAla----- 1175

Db       3705 TGATGAGGAAGATCGCTTCCATGGTGTGCGCCTGCAGACTTCGCCCCCAATGGAACCCCT 3764

Qy       1176 -------GlyThrGluHis-----------------------------------LysGl 1181

Db       3765 GAACTTTGGTTCCAGTTATATTGTGTCTAATTCTGCTAACCTGAAAGTAATGCCCAAGGA 3824

Qy       1181 nAspLysMet----------------------------LeuSerValGlyTyrSerGl 1191

Db       3825 GTTGAAATTGTCCTACAGGAGCCCTGGAGAAATTCAGCACTTCTCAAAATTCTATGCTGG 3884

Qy       1191 yAlaTrpSerGluThrAlaGluLeuGluGlyLeuGlySerAsnSerAlaAspHisAspHi 1211

Db       3885 GCAGATGAAGGAACCCATTCAACTTGAG--------------ATTACTGAAAAAAGACA 3929

Qy       1211 sGlyGlyMetAlaTrpSerLeuGlyArgGluLeuSerSerArgGlyLeuCys-------- 1228

Db       3930 TGGGACTTTGGTGTGGGATACTGA-GGTGAAGCCAGTGGATCTCCAGCTTGTAGCTGCAT 3988

Qy       1229 ----ProThrValLeuMetThrThrAlaValCysProGly 1240

Db       3989 CAGCCCCTCCTCCTTTCTCAGGTGCAGCCTTTGTGAAGGA 4028
```

RESULT 5
US-09-388-221B-9
; Sequence 9, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 4556
; TYPE: DNA

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(4365)
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Construct
US-09-388-221B-9

Alignment Scores:
Pred. No.:                5.09e-90        Length:         4556
Score:                    945.50          Matches:        363
Percent Similarity:       37.97%          Conservative:   208
Best Local Similarity:    24.14%          Mismatches:     525
Query Match:              13.37%          Indels:         410
DB:                       4               Gaps:           47

US-10-066-521-6 (1-1344) x US-09-388-221B-9 (1-4556)

Qy          11 SerTyrGlyLeuGlnTrpCysLeuTyrGlu---LeuAspLysGluGluPheGlnThrPhe  29
               ::::::|||         |||      |||   |||   |||||||||   :::  |||
Db          13 GCCTGGGGCCGCCTGGCCTGTTACTTGGAGTTCCTGAAGAAGGAGGAGCTGAAGGAGTTC  72

Qy          30 LysGluLeuLeuLysLysLysSer---SerGluSerThrThrCysSerIleProGlnPhe  48
               :::   ||||||      |||:::   |||   |||::::::         |||
Db          73 CAGCTTCTGCTCGCCAATAAAGCGCACTCCAGGAGCTCTTCGGGTGAGACACCCGCTCAG 132

Qy          49 GluIleGluAsnAlaAsnValGluCysLeuAlaLeuLeuLeuHisGluTyrTyrGlyAla  68
                  :::   :::   :::|||      :::   |||:::   :::   ||||||
Db         133 CCAGAGAAGACGAGTGGCATGGAGGTGGCCTCGTACCTGGTGGCTCAG---TATGGGGAG 189

Qy          69 SerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArgThrLeuSer  88
               ||||||    ::::::     :::|||   |||   |||||:::|||
Db         190 CAGCGGGCCTGGGACCTAGCCCTCCATACCTGGGAGCAGATGGGGCTGAGGTCACTGTGC 249

Qy          89 GluLysAlaArgAspAsp------------------------------------------  94
                  :::|||::::::
Db         250 GCCCAAGCCCAGGAAGGGGCAGGCCACTCTCCCTCATTCCCCTACAGCCCAAGTGAACCC 309

Qy          94 ------------------------------------------------------------  94

Db         310 CACCTGGGGTCTCCCAGCCAACCCACCTCCACCGCAGTGCTAATGCCCTGGATCCATGAA 369

Qy          94 ------------------------------------------------------------  94

Db         370 TTGCCGGCGGGGTGCACCCAGGGCTCAGAGAGAAGGGTTTTGAGACAGCTGCCTGACACA 429

Qy          95 -----------MetLysLysIleSerGlnAlaMet----------------------- 102
                         ::::::||||||   ::::::
Db         430 TCTGGACGCCGCTGGAGAGAAATCTCTGCCTCACTCCTCTACCAAGCTCTTCCAAGCTCC 489

Qy         102 ------------------------------------------------------------ 102

Db         490 CCAGACCATGAGTCTCCAAGCCAGGAGTCACCCAACGCCCCCACATCCACAGCAGTGCTG 549

Qy         103 ----------------------------------------GluGlnGluGlyAla--- 107
                                                       |||||||||
Db         550 GGGAGCTGGGGATCCCCACCTCAGCCCAGCCTAGCACCCAGAGAGCAGGAGGCTCCTGGG 609

Qy         108 -------------------------------------ThrAlaAlaGluThrGluGlu 114
                                                    |||                |||
Db         610 ACCCAATGGCCTCTGGATGAAACGTCAGGAATTTACTACACAGAAATCAGAGAAAGAGAG 669

Qy         115 GlnGluIleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGln 134
               :::|||   |||:::                |||             |||      |||
Db         670 AGAGAGAAATCAGAGAAAGGCAGGCCCCCATGGGCAGCGGTGGTAGGAACGCCCCCACAG 729

Qy         135 GlyHisGlyGly------------------------------------------------ 138
                  |||
Db         730 GCGCACACCAGCCTACAGCCCCACCACCACCCATGGGAGCCTTCTGTGAGAGAGAGCCTC 789

Qy         139 ---AspThrTrpAspTyrLysSerHisValMetThr---LysPhe-------------- 151
                  ||||||   :::|||:::                |||||
```

```
Db         790 TGTTCCACATGGCCCTGGAAAAATGAGGATTTTAACCAAAAATTCACACAGCTGCTACTT 849

Qy         152 ---------------------AlaGluGluGluAspValArgArgSerPheGluAsnThr 164
                                   :::::::::      |||:::||||||
Db         850 CTACAAAGACCTCACCCCAGAAGCCAAGATCCCCTGGTCAAGAGAAGC------------ 897

Qy         165 AlaAlaAspTrpPro---------------------------------GluMetGlnThr 173
                     ||||||                                  |||::::::
Db         898 ---------TGGCCTGATTATGTGGAGGAGAATCGAGGACATTTAATTGAGATCAGAGAC 948

Qy         174 LeuAlaGly---AlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeu 192
               |||   |||         |||:::                  ||||||   |||:::|||
Db         949 TTATTTGGCCCAGGCCTGGATACCCAA------------GAACCTCGCATAGTCATACTG 996

Qy         193 HisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAla 212
                  |||   :::|||||||||||||||   ||||||||::::::          |||
Db         997 CAGGGGGCTGCTGGAATTGGGAAGTCAACACTGGCCAGGCAGGTGAAGGAAGCCTGGGGG 1056

Qy         213 GlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMet 232
               :::|||   ||||||         |||   :::||||||:::         ||||||:::
Db        1057 AGAGGCCAGCTGTATGGGGACCGCTTCCAGCATGTCTTCTACTTCAGCTGCAGAGAGCTG 1116

Qy         233 GlnArgLysLysGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGln 252
                  :::   |||       |||:::   |||   |||   ::::::         :::
Db        1117 GCCCAGTCCAAGGTGGTGAGTCTCGCTGAGCTCATCGGAAAAGATGGGACAGCCACTCCG 1176

Qy         253 AlaProValThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPhe 272
               ||||||:::   :::|||:::||||||||||||||||||||||||||:::||||||
Db        1177 GCTCCCATTAGACAGATCCTGTCTAGGCCAGAGCGGCTGCTCTTCATCCTCGATGGTGTA 1236

Qy         273 AspAspLeuGlySerValLeuAsnAsn---AspThrLysLeuCysLysAspTrpAlaGlu 291
               |||:::   |||   ||||||         ::::::||||||      |||::::::
Db        1237 GATGAGCCAGGATGGGTCTTGCAGGAGCCGAGTTCTGAGCTCTGTCTGCACTGGAGCCAG 1296

Qy         292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSer 311
                  ||||||         |||:::   |||||||||   |||   :::|||||||||:::
Db        1297 CCACAGCCGGCGGATGCACTGCTGGGCAGTTTGCTGGGGAAAACTATACTTCCCGAGGCA 1356

Qy         312 PheLeuIleValThrValArgAspValGlyThrGluLysLeuLysSerGluValValSer 331
                  ::::::|||   |||         :::   |||         :::
Db        1357 TCCTTCCTGATCACGGCTCGGACCACAGCTCTGCAGAACCTCATTCCTTCTTTGGAGCAG 1416

Qy         332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGlu 351
                  |||::::::   |||   |||   |||         |||
Db        1417 GCACGTTGGGTAGAGGTCCTGGGGTTCTCTGAGTCCAGCAGGAAGGAATATTTCTACAGA 1476

Qy         352 ArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGlu 371
                     |||   |||   :::       |||   :::   :::|||:::|||
Db        1477 TATTTCACAGATGAAAGGCAAGCAATTAGAGCCTTTAGGTTGGTCAAATCAAACAAAGAG 1536

Qy         372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu 391
               |||         |||   |||||||   |||       |||   |||       |||
Db        1537 CTCTGGGCCCTGTGTCTTGTGCCCTGGGTGTCCTGGCTGGCCTGCACTTGCCTGATGCAG 1596

Qy         392 GlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeuThrGly------Leu 409
               |||             |||   :::         :::::|||   |||         |||
Db        1597 CAGATGAAGCGGAAGGAAAAACTCACACTGACTTCCAAGACCACCACAACCCTCTGTCTA 1656

Qy         410 HisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsn 429
               |||             |||   |||   |||
Db        1657 CATTACCTTGCCCAGGCTCTCCAAGCTCAGCCATTGGGA---------------------- 1695

Qy         430 LeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsn 449
                           |||:::      |||   :::|||   ||||||:::|||
Db        1696 ------------CCCCAGCTCAGAGACCTCTGCTCTCTGGCTGCTGAGGGCATCTGGCAA 1743

Qy         450 ArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeu 469
               :::|||::::::|||         |||||||||         ||||||   :::   :::
Db        1744 AAAAAGACCCTTTTCAGTCCAGATGACCTCAGGAAGCATGGGTTAGATGGGGCCATCATC 1803

Qy         470 ArgAlaLeuPheHisMetAsnIleLeu------------LeuProAspSerHisCysGlu 485
                        |||   ||||||         :::|||   |||
Db        1804 TCCACCTTCTTGAAGATGGGTATTCTTCAAGAGCACCCCATCCCTCTGAGC--------- 1854
```


Qy 486 GluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrVal 505
Db 1855 ------TACAGCTTCATTCACCTCTGTTTCCAAGAGTTCTTTGCAGCAATGTCCTATGTC 1908
Qy 506 LeuGluGlyLeuGlu------IleGluProAlaLeuCysProLeuTyrValGluLysThr 523
Db 1909 TTGGAGGATGAGAAGGGGAGAGGTAAACATTCTAATTGCATCATAGATTTGGAAAAGACG 1968
Qy 524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp--------- 540
Db 1969 CTAGAAGCA--------------------TATGGAATACATGGCCTGTTTGGGGCATCA 2007
Qy 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560
Db 2008 ACCACACGTTTCCTATTGGGCCTGTTAAGTGATGAGGGGGAGAGAGAGATGGAGAACATC 2067
Qy 561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeu 580
Db 2068 TTTCACTGCCGGCTGTCTCAGGGG------AGGAACCTGATGCAGTGGGTCCCGTCCCTG 2121
Qy 581 Gly------GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCys 598
Db 2122 CAGCTGCTGCTGCAGCCACAC----------------TCTCTGGAGTCCCTCCACTGC 2163
Qy 599 LeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618
Db 2164 TTGTACGAGACTCGGAACAAAACGTTCCTGACACAAGTGATGGCCCATTTCGAAGAAATG 2223
Qy 619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCys 638
Db 2224 GGCATGTGTGTAGAAACAGACATGGAGCTCTTAGTGTGCACTTTCTGCATTAAATTCAGC 2283
Qy 639 ProTyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerAla 658
Db 2284 CGCCACGTGAAGAAGCTTCAGCTG---ATTGAGGGC---------AGGCAGCACAGATCA 2331
Qy 659 GluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrp 678
Db 2332 ACATGGAGCCCCACCATGGTAGTCCTGTTCAGGTGGGTCCCAGTCACAGATGCCTATTGG 2391
Qy 679 GluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySer 698
Db 2391 -- 2391
Qy 699 SerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCys 718
Db 2391 -- 2391
Qy 719 LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrp 738
Db 2392 --CAGATTCTCTTC 2403
Qy 739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLys 758
Db 2404 TCCGTCCTCAAGGTCACCAGAAACCTGAAGGAGCTGGACCTAAGTGGAAACTCGCTGAGC 2463
Qy 759 GluGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSer 778
Db 2464 CACTCTGCAGTGAAGAGTCTTTGTAAGACCCTGAGACGCCCTCGCTGCCTCCTGGAGACC 2523
Qy 779 LeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeu 798
Db 2524 CTGCGGTTGGCTGGCTGTGGCCTCACAGCTGAGGACTGCAAGGACCTTGCCTTTGGGCTG 2583
Qy 799 ThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGly 818
Db 2584 AGAGCCAACCAGACCCTGACCGAGCTGGACCTGAGCTTCAATGTGCTCACGGATGCTGGA 2643
Qy 819 ValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeu 838
Db 2644 GCCAAACACCTTTGCCAGAGACTGAGACAGCCGAGCTGCAAGCTACAGCGACTGCAGCTG 2703
Qy 839 GluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsn 858
Db 2704 GTCAGCTGTGGCCTCACGTCTGACTGCTGCCAGGACCTGGCCTCTGTGCTTAGTGCCAGC 2763
Qy 859 ArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeu 878
Db 2764 CCCAGCCTGAAGGAGCTAGACCTGCAGCAGAACAACCTGGATGACGTTGGCGTGCGACTG 2823
Qy 879 LeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCys 898
Db 2824 CTCTGTGAGGGGCTCAGGCATCCTGCCTGCAAACTCATACGCCTGGGGCTGGACCAGACA 2883
Qy 899 HisLeuAsp-- 901
Db 2884 ACTCTGAGTGATGAGATGAGGCAGGAACTGAGGGCCCTGGAGCAGGAGAAACCTCAGCTG 2943
Qy 902 ------------------------------------ThrAlaGlyCysGlyPheLeu 908
Db 2944 CTCATCTTCAGCAGACGGAAACCAAGTGTGATGACCCCTACTGAGGGC---------CTG 2994
Qy 909 AlaLeuAlaLeuMetGlyAsnSerTrp------LeuThrHisLeuSerLeu--------- 923
Db 2995 GATACGGGAGAGATGAGTAATAGCACATCCTCACTCAAGCGGCAGAGACTCGGATCAGAG 3054
Qy 924 ---SerMetAsnProValGluAspAsnGlyValLysLeuLeu----------------- 936
Db 3055 AGGGCGGCTTCCCATGTTGCTCAGGCTAATCTCAAACTCCTGGACGTGAGCAAGATCTTC 3114
Qy 937 ------CysGluValMetArgGluProSerCysHisLeuGlnAspLeuGluLeuVal-Ly 954
Db 3115 CCAATTGCTGAGATTGCAGAGGAAAGCTCCCCAGAGGTAGTACCGGTGGAACTCTTGTGC 3174
Qy 954 sCys---------HisLeuThrAlaAlaCysCysGluSerLeuSerCysValIleSerAr 971
Db 3175 GTGCCTTCTCCTGCCTCTCAAGGGGACCTGCATACGAAGCCTTTGGGGACTGACGATGAC 3234
Qy 971 gSerArgHisLeuLysSerLeuAspLeu-----------------------ThrAspAs 983
Db 3235 TTTCTGGGGCCTGAAGGAAATGTGGATGTTGAGTTGATTGATAAGAGCACAAACAGATAC 3294
Qy 983 nAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGlu----------------------- 995
Db 3295 AGCGTTTGGTTCCCCACTGCTGGCTGGTATCTGTGGTCAGCCACAGGCCTCGGCTTCCTG 3354
Qy 996 ----GlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLe 1014
Db 3355 GTAAGGGATGAGGTCACAGTGACGATTGCGTTTGGTTCCTGGAGTCAGCACCTGGCCCTG 3414
Qy 1014 uThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSe 1034
Db 3415 GACCTGCAGCACCATGAACAGTGGCTGGTGGGCGGCCCCTTGTTTGATGTCACTGCAGAG 3474
Qy 1034 rLeuAsnLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCysSer----- 1052
Db 3475 C------------CAGAGGAGGCTGTCGCCGAAATCCACCTCCCCCACTTCATCTCCCTC 3522
Qy 1053 -------AlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeu------TrpLy 1068
Db 3523 CAAGGTGAGGTGGACGTCTCCTGGTTTCTCGTTGCCCATTTTAAGAATGAAGGGATGGTC 3582
Qy 1068 sTrpGlnTyrProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuLysProAr 1088
Db 3583 CTGGAG-CATCCAGCCCGGGTGGAGCCTTTCTATGCTGTCCTGGAA------AGCCCCAG 3635
Qy 1088 gValValIleAspGlySerTrpHisSerPheAspGluAspAspArgHisLysIleGlyLe 1108
Db 3636 CTTCTCTCTGATGGGCATCCTGCTGCGGATCGCCAGTGGGACTCGCCTCTCCATCCCCAT 3695
Qy 1108 uThrPheArgLeuProGluSerArgAlaTrpProCysAlaLeuLeuTrpGlyMetAsnPr 1128
Db 3696 CACTTCCAAC----------------------ACATTGATCTATTATCACCCCCACCC 3731
Qy 1128 oGluGln---LysLysArgValSerLeuLeuAlaGlyAspPheLysSerSerThrArgPh 1147

```
Db       3732 CGAAGATATTAAGTTCCACTTGTACCTTGTCCCCAGCGAC-------------------- 3771

Qy       1147 eAlaLysSerLeuCysLeuAlaThrAlaAsnGlyGluSerGlnArgValAspAsnValGl 1167

Db       3772 -------GCCTTGCTAACAAAGGCGATAGATGATGAGGAAGATCGCTTCCATGGTGTGCG 3824

Qy       1167 uGlnSerSerProGlnProMetAla------------GlyThrGluHis----------- 1179

Db       3825 CCTGCAGACTTCGCCCCCAATGGAACCCCTGAACTTTGGTTCCAGTTATATTGTGTCTAA 3884

Qy       1180 -------------------------LysGlnAspLysMet-------------------- 1184

Db       3885 TTCTGCTAACCTGAAAGTAATGCCCAAGGAGTTGAAATTGTCCTACAGGAGCCCTGGAGA 3944

Qy       1185 ----------LeuSerValGlyTyrSerGlyAlaTrpSerGluThrAlaGluLeuGluGl 1201

Db       3945 AATTCAGCACTTCTCAAAATTCTATGCTGGGCAGATGAAGGAACCCATTCAACTTGAG-- 4002

Qy       1201 yLeuGlySerAsnSerAlaAspHisAspHisGlyGlyMetAlaTrpSerLeuGlyArgGl 1221

Db       4003 ------------ATTACTGAAAAAAGACATGGGACTTTGGTGTGGGATACTGA-GGTGA 4048

Qy       1221 uLeuSerSerArgGlyLeuCys------------ProThrValLeuMetThrThrAlaVa 1237

Db       4049 AGCCAGTGGATCTCCAGCTTGTAGCTGCATCAGCCCCTCCTCCTTTCTCAGGTGCAGCCT 4108

Qy       1237 lCysProGly 1240

Db       4109 TTGTGAAGGA 4118

RESULT 6
US-08-910-731-3
; Sequence 3, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1374 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1368
US-08-910-731-3

Alignment Scores:
Pred. No.:                4.28e-57      Length:          1374
Score:                    630.50        Matches:         151
Percent Similarity:       51.38%        Conservative:    73
Best Local Similarity:    34.63%        Mismatches:      205
Query Match:              8.91%         Indels:          9
DB:                       2             Gaps:            3

US-10-066-521-6 (1-1344) x US-08-910-731-3 (1-1374)

Qy        653 ProArgAspGluSerAlaGluAlaCysProValValProLeuTrpMetArg------Asp 670

Db         39 CCGGTGGACAGAGCTCCTTCCCCTGATCCAACAATACCAAG-TGGTC-AGGCTGGATGAC 96

Qy        671 LysThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGlyThrHisProHis 690

Db         97 TGTGGCCTCACTGAAGTGCGGTGCAAAGACATCAGGTCAGCGATCCAGGCCAACCCTGCC 156

Qy        691 LeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLysThrLeuCys 710

Db        157 CTGACAGAGCTCAGCCTACGCACCAATGAACTGGGTGATGCTGGTGTGGGTCTGGTGCTC 216

Qy        711 AlaLysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIle 730

Db        217 CAGGGCCTGCAGAATCCCACTTGTAAGATCCAGAAGCTGAGCCTTCAGAACTGCAGCTTG 276

Qy        731 Thr---ProGlyValGlnHisLeuTrpArgIleValMetAlaAsnArgAsnLeuArgSer 749

Db        277 ACGGAAGCTGGCTGTGGGGTCCTGCCTGATGTGCTGCGCTCTTTGTCTACCCTGCGTGAA 336

Qy        750 LeuAsnLeuGlyGlyThrHisLeuLysGluGluAspValArgMetAlaCysGluAlaLeu 769

Db        337 CTACATCTCAATGACAACCCTCTGGGGGATGAAGGCCTGAAGCTGCTCTGTGAAGGACTC 396

Qy        770 LysHisProLysCysLeuLeuGluSerLeuArgLeuAspCysCysGlyLeuThrHisAla 789

Db        397 CGGGACCCCCAGTGCCGTCTTGAGAAGCTTCAGTTGGAATACTGTAACCTCACAGCTACC 456

Qy        790 CysTyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeu 809

Db        457 AGCTGCGAGCCCCTGGCCTCAGTGCTCAGGGTGAAACCTGACTTTAAAGAGCTAGTATTG 516

Qy        810 AlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgValSer 829

Db        517 AGCAACAATGACTTCCATGAGGCTGGTATCCACACTCTGTGCCAGGGCCTGAAGGATTCT 576

Qy        830 GlnCysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAlaThrGlyCysGln 849

Db        577 GCCTGTCAACTGGAGTCACTCAAACTGGAGAACTGTGGTATCACATCAGCCAACTGCAAG 636

Qy        850 SerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsn 869

Db        637 GATCTGTGTGATGTTGTGGCCTCCAAAGCCTCACTGCAAGAACTGGACTTGGGCAGCAAC 696

Qy        870 SerLeuGlyAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCysSer 889

Db        697 AAGCTGGGCAACACAGGCATTGCAGCACTGTGCTCAGGACTGCTGCTTCCCAGCTGCAGG 756

Qy        890 LeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAla 909

Db        757 CTGAGGACTCTGTGGCTCTGGGACTGTGATGTCACTGCAGAAGGCTGCAAGGACCTGTGC 816
```

```
Qy        910 LeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProValGlu 929
Db        817 CGTGTCCTCAGAGCCAAGCAGAGCCTGAAGGAACTCAGCCTAGCTGGCAATGAGCTGAAG 876

Qy        930 AspAsnGlyValLysLeuLeuCysGluValMetArgGluProSerCysHisLeuGlnAsp 949
Db        877 GATGAGGGTGCCCAACTGCTGTGTGAGAGCCTGTTAGAGCCTGGCTGTCAGCTGGAGTCA 936

Qy        950 LeuGluLeuValLysCysHisLeuThrAlaAlaCysCysGluSerLeuSerCysValIle 969
Db        937 CTGTGGGTAAAGACCTGTAGCCTCACAGCTGCCTCTTGTCCCCACTTCTGCTCGGTGTTG 996

Qy        970 SerArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGly 989
Db        997 ACCAAAAACAGTTCTCTGTTTGAGTTGCAAATGAGCAGCAACCCGCTGGGAGACTCGGGA 1056

Qy        990 ValAlaAlaLeuCysGluGlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeu 1009
Db       1057 GTCGTGGAGCTTTGCAAGGCCCTGGGCTATCCGGACACAGTGCTGCGTGTGCTTTGGCTG 1116

Qy       1010 LysAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsn 1029
Db       1117 GGAGACTGTGATGTGACAGACAGTGGCTGCAGCAGCCTTGCCACTGTCCTGCTGGCCAAC 1176

Qy       1030 ArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGlyMetMetLys 1049
Db       1177 CGCAGCTTGAGGGAACTGGACCTCAGTAACAACTGCATGGGGGACAACGGTGTCCTACAA 1236

Qy       1050 LeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeu--------- 1066
Db       1237 CTGCTGGAGAGCCTCAAACAGCCCAGCTGCATCCTTCAGCAGCTTGTCCTGTATGACATT 1296

Qy       1067 ---TrpLysTrpGlnTyrProValGlnIleArgLysLeuGluGlu 1081
Db       1297 TACTGGACGGATGAGGTGGAAGACCAGCTTCGGGCCCTGGAGGAGGAA 1344
```

RESULT 7
US-08-795-395-3
; Sequence 3, Application US/08795395
; Patent No. 5965399
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Cloning and Expression of Rat Liver and
; TITLE OF INVENTION: Porcine Liver Ribonuclease Inhibitor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,395
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1374 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
US-08-795-395-3

Alignment Scores:

Pred. No.:	4.28e-57	Length:	1374
Score:	630.50	Matches:	151
Percent Similarity:	51.38%	Conservative:	73
Best Local Similarity:	34.63%	Mismatches:	205
Query Match:	8.91%	Indels:	9
DB:	2	Gaps:	3

US-10-066-521-6 (1-1344) x US-08-795-395-3 (1-1374)

```
Qy        653 ProArgAspGluSerAlaGluAlaCysProValValProLeuTrpMetArg------Asp 670
Db         39 CCGGTGGACAGAGCTCCTTCCCCTGATCCAACAATACCAAG-TGGTC-AGGCTGGATGAC 96

Qy        671 LysThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGlyThrHisProHis 690
Db         97 TGTGGCCTCACTGAAGTGCGGTGCAAAGACATCAGGTCAGCGATCCAGGCCAACCCTGCC 156

Qy        691 LeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLysThrLeuCys 710
Db        157 CTGACAGAGCTCAGCCTACGCACCAATGAACTGGGTGATGCTGGTGTGGGTCTGGTGCTC 216

Qy        711 AlaLysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIle 730
Db        217 CAGGGCCTGCAGAATCCCACTTGTAAGATCCAGAAGCTGAGCCTTCAGAACTGCAGCTTG 276

Qy        731 Thr---ProGlyValGlnHisLeuTrpArgIleValMetAlaAsnArgAsnLeuArgSer 749
Db        277 ACGGAAGCTGGCTGTGGGGTCCTGCCTGATGTGCTGCGCTCTTTGTCTACCCTGCGTGAA 336

Qy        750 LeuAsnLeuGlyGlyThrHisLeuLysGluGluAspValArgMetAlaCysGluAlaLeu 769
Db        337 CTACATCTCAATGACAACCCTCTGGGGGATGAAGGCCTGAAGCTGCTCTGTGAAGGACTC 396

Qy        770 LysHisProLysCysLeuLeuGluSerLeuArgLeuAspCysCysGlyLeuThrHisAla 789
Db        397 CGGGACCCCCAGTGCCGTCTTGAGAAGCTTCAGTTGGAATACTGTAACCTCACAGCTACC 456

Qy        790 CysTyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeu 809
Db        457 AGCTGCGAGCCCCTGGCCTCAGTGCTCAGGGTGAAACCTGACTTTAAAGAGCTAGTATTG 516

Qy        810 AlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgValSer 829
Db        517 AGCAACAATGACTTCCATGAGGCTGGTATCCACACTCTGTGCCAGGGCCTGAAGGATTCT 576

Qy        830 GlnCysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAlaThrGlyCysGln 849
Db        577 GCCTGTCAACTGGAGTCACTCAAACTGGAGAACTGTGGTATCACATCAGCCAACTGCAAG 636

Qy        850 SerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsn 869
Db        637 GATCTGTGTGATGTTGTGGCCTCCAAAGCCTCACTGCAAGAACTGGACTTGGGCAGCAAC 696

Qy        870 SerLeuGlyAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCysSer 889
Db        697 AAGCTGGGCAACACAGGCATTGCAGCACTGTGCTCAGGACTGCTGCTTCCCAGCTGCAGG 756

Qy        890 LeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAla 909
Db        757 CTGAGGACTCTGTGGCTCTGGGACTGTGATGTCACTGCAGAAGGCTGCAAGGACCTGTGC 816
```

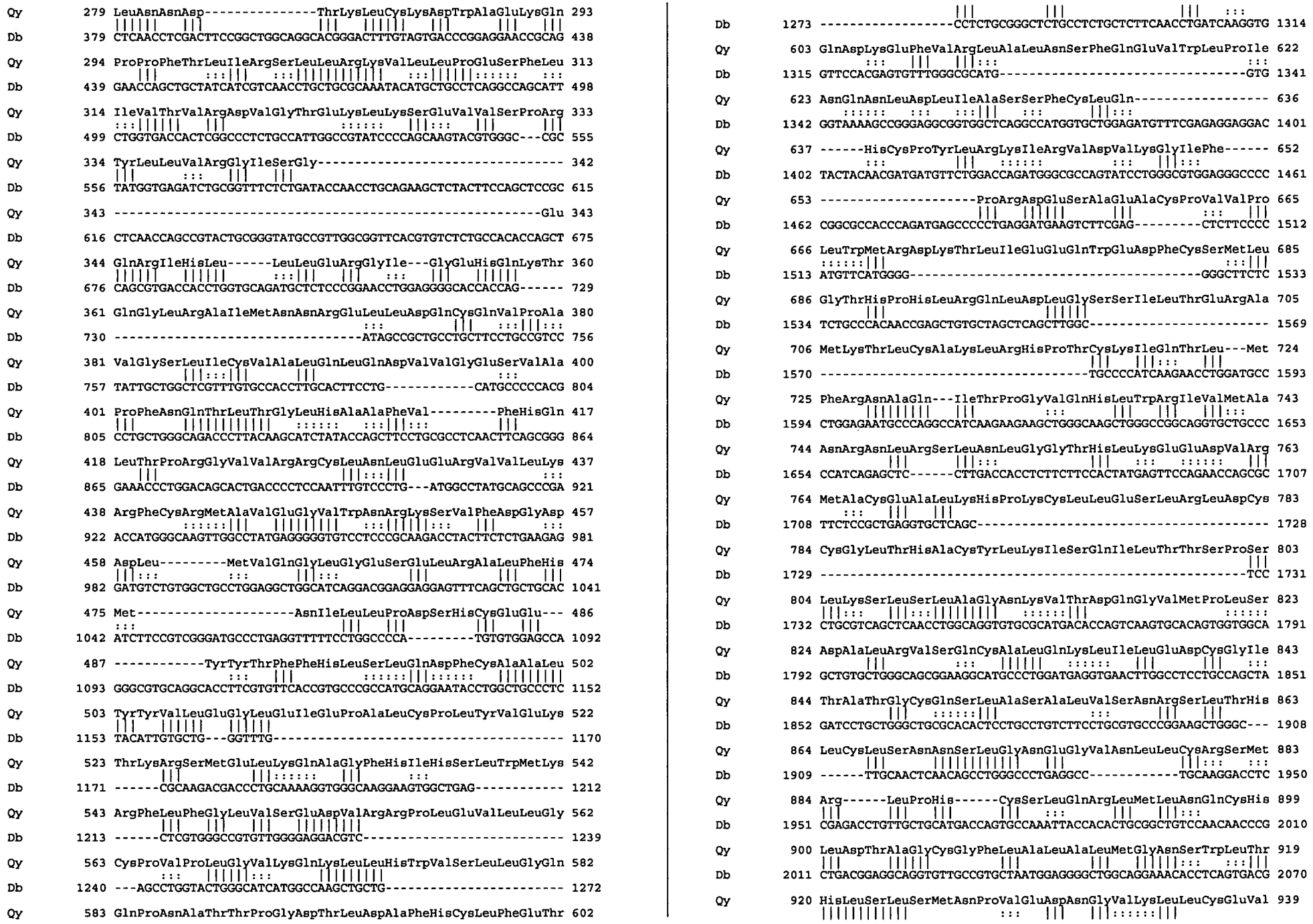
```
Qy        910 LeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProValGlu 929
Db        817 CGTGTCCTCAGAGCCAAGCAGAGCCTGAAGGAACTCAGCCTAGCTGGCAATGAGCTGAAG 876

Qy        930 AspAsnGlyValLysLeuLeuCysGluValMetArgGluProSerCysHisLeuGlnAsp 949
Db        877 GATGAGGGTGCCCAACTGCTGTGTGAGAGCCTGTTAGAGCCTGGCTGTCAGCTGGAGTCA 936

Qy        950 LeuGluLeuValLysCysHisLeuThrAlaAlaCysCysGluSerLeuSerCysValIle 969
Db        937 CTGTGGGTAAAGACCTGTAGCCTCACAGCTGCCTCTTGTCCCCACTTCTGCTCGGTGTTG 996

Qy        970 SerArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGly 989
Db        997 ACCAAAAACAGTTCTCTGTTTGAGTTGCAAATGAGCAGCAACCCGCTGGGAGACTCGGGA 1056

Qy        990 ValAlaAlaLeuCysGluGlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeu 1009
Db       1057 GTCGTGGAGCTTTGCAAGGCCCTGGGCTATCCGGACACAGTGCTGCGTGTGCTTTGGCTG 1116

Qy       1010 LysAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsn 1029
Db       1117 GGAGACTGTGATGTGACAGACAGTGGCTGCAGCAGCCTTGCCACTGTCCTGCTGGCCAAC 1176

Qy       1030 ArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGlyMetMetLys 1049
Db       1177 CGCAGCTTGAGGGAACTGGACCTCAGTAACAACTGCATGGGGGACAACGGTGTCCTACAA 1236

Qy       1050 LeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeu--------- 1066
Db       1237 CTGCTGGAGAGCCTCAAACAGCCCAGCTGCATCCTTCAGCAGCTTGTCCTGTATGACATT 1296

Qy       1067 ---TrpLysTrpGlnTyrProValGlnIleArgLysLeuLeuGluGlu 1081
Db       1297 TACTGGACGGATGAGGTGGAAGACCAGCTTCGGGCCCTGGAGGAGGAA 1344

RESULT 8
US-08-910-731-1
; Sequence 1, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1371 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1368
US-08-910-731-1

Alignment Scores:
Pred. No.:                4.49e-56      Length:          1371
Score:                    621.00        Matches:         151
Percent Similarity:       50.11%        Conservative:    86
Best Local Similarity:    31.92%        Mismatches:      210
Query Match:              8.78%         Indels:          26
DB:                       2             Gaps:            5

US-10-066-521-6 (1-1344) x US-08-910-731-1 (1-1371)

Qy        625 AsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIle 644
Db          4 AACCTCGATATT----------------------CATTGCGAGCAGCTGAGCGACGCC 39

Qy        645 ArgValAspValLysGlyIleProArgAspGluSerAlaGluAlaCysProValVal 664
Db         40 CGG-------------------------------TGGACAGAGCTCCTGCCGCTGCTC 66

Qy        665 ProLeuTrp------------MetArgAspLysThrLeuIleGluGluGlnTrpGluAsp 680
Db         67 CAGCAGTATGAGGTGGTCAGGCTCGACGACTGCGGCCTCACGGAGGAGCACTGCAAGGAC 126

Qy        681 PheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIle 700
Db        127 ATCGGTTCTGCCCTCCGGGCCAACCCCTCCCTGACCGAGCTCTGCCTCCGCACCAACGAG 186

Qy        701 LeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCysLysIle 720
Db        187 CTGGGCGATGCCGGCGTGCACCTGGTGCTGCAGGGCCTGCAGAGCCCCACCTGCAAGATC 246

Qy        721 GlnThrLeuMetPheArgAsnAlaGlnIleThr---ProGlyValGlnHisLeuTrpArg 739
Db        247 CAGAAGCTCAGCCTGCAGAACTGCTCCCTGACCGAGGCGGGCTGCGGGGTCCTGCCCAGC 306

Qy        740 IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGlu 759
Db        307 ACGCTGCGCTCCCTGCCCACGCTGCGGGAGCTGCATCTCAGCGACAACCCACTGGGGGAC 366

Qy        760 GluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSerLeu 779
Db        367 GCCGGCCTGCGGCTGCTCTGTGAGGGGCTCCTGGACCCCCAGTGCCACCTGGAGAAGCTG 426

Qy        780 ArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThr 799
Db        427 CAGTTGGAGTACTGCCGCCTGACGGCCGCCAGCTGCGAGCCCCTGGCCTCGGTGCTCAGG 486

Qy        800 ThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyVal 819
Db        487 GCCACGCGGGCCTTGAAGGAGCTCACGGTGAGCAACAACGACATCGGCGAGGCCGGCGCC 546

Qy        820 MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGlu 839
Db        547 CGGGTGCTGGGCCAGGGTCTGGCAGACTCTGCCTGCCAGCTGGAGACGCTCAGGCTGGAG 606

Qy        840 AspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
Db        607 AACTGCGGTCTCACGCCAGCCAACTGCAAAGACCTGTGCGGAATTGTGGCCTCCCAGGCC 666
```

```
Qy        860 SerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeu 879
Db        667 TCGCTGAGGGAGCTTGACCTGGGCAGCAACGGGCTGGGCGACGCGGGCATAGCCGAGCTG 726

Qy        880 CysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899
Db        727 TGCCCCGGGCTCTTGAGCCCCGCCTCCCGCCTCAAGACCCTGTGGCTCTGGGAGTGTGAC 786

Qy        900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThr 919
Db        787 ATCACCGCCAGTGGCTGCAGAGACCTCTGCCGTGTCCTCCAGGCCAAGGAGACCCTGAAG 846

Qy        920 HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGluVal 939
Db        847 GAGCTCAGTCTGGCGGGCAACAAGCTGGGCGACGAGGGCGCCCGGCTGCTGTGCGAGAGC 906

Qy        940 MetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThrAla 959
Db        907 CTGCTGCAGCCCGGCTGCCAGCTGGAGTCCCTGTGGGTGAAGTCCTGCAGCCTCACGGCG 966

Qy        960 AlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAsp 979
Db        967 GCCTGCTGCCAGCACGTCAGCTTGATGCTGACCCAGAACAAGCATCTCCTGGAACTTCAG 1026

Qy        980 LeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGln 999
Db       1027 TTGAGCAGCAACAAGCTGGGTGACTCTGGCATCCAGGAGCTGTGCCAGGCCCTGAGCCAG 1086

Qy       1000 LysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCys 1019
Db       1087 CCGGGCACCACACTGCGGGTGCTCTGTCTTGGGGACTGTGAGGTGACCAACAGCGGCTGC 1146

Qy       1020 GluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGln 1039
Db       1147 AGCAGCCTCGCCTCGCTCCTGCTGGCCAACCGCAGCCTGCGAGAGCTGGACCTGAGCAAC 1206

Qy       1040 AsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSer 1059
Db       1207 AACTGTGTGGGCGACCCGGGCGTCCTGCAGCTGCTGGGGAGCCTGGAGCAGCCGGGCTGC 1266

Qy       1060 AsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleArgLysLeuLeu 1079
Db       1267 GCCCTGGAGCAGCTGGTCCTGTACGACACCTACTGGACGGAGGAGGTGGAGGACCGCCTG 1326

Qy       1080 GluGluValGlnLeuLeuLysPro------ArgValVal 1090
Db       1327 CAGGCCCTGGAGGGGAGCAAGCCCGGCCTGAGGGTCATC 1365

RESULT 9
US-08-795-395-1
; Sequence 1, Application US/08795395
; Patent No. 5965399
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Cloning and Expression of Rat Liver and
;    TITLE OF INVENTION:  Porcine Liver Ribonuclease Inhibitor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,395
;      FILING DATE:  04-FEB-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1371 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1368
US-08-795-395-1

Alignment Scores:
Pred. No.:                4.49e-56        Length:          1371
Score:                    621.00          Matches:         151
Percent Similarity:       50.11%          Conservative:    86
Best Local Similarity:    31.92%          Mismatches:      210
Query Match:              8.78%           Indels:          26
DB:                       2               Gaps:            5

US-10-066-521-6 (1-1344) x US-08-795-395-1 (1-1371)

Qy        625 AsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIle 644
Db          4 AACCTCGATATT----------------------CATTGCGAGCAGCTGAGCGACGCC 39

Qy        645 ArgValAspValLysGlyIleProArgAspGluSerAlaGluAlaCysProValVal 664
Db         40 CGG--------------------------------TGGACAGAGCTCCTGCCGCTGCTC 66

Qy        665 ProLeuTrp-----------MetArgAspLysThrLeuIleGluGluGlnTrpGluAsp 680
Db         67 CAGCAGTATGAGGTGGTCAGGCTCGACGACTGCGGCCTCACGGAGGAGCACTGCAAGGAC 126

Qy        681 PheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIle 700
Db        127 ATCGGTTCTGCCCTCCGGGCCAACCCCTCCCTGACCGAGCTCTGCCTCCGCACCAACGAG 186

Qy        701 LeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCysLysIle 720
Db        187 CTGGGCGATGCCGGCGTGCACCTGGTGCTGCAGGGCCTGCAGAGCCCCACCTGCAAGATC 246

Qy        721 GlnThrLeuMetPheArgAsnAlaGlnIleThr---ProGlyValGlnHisLeuTrpArg 739
Db        247 CAGAAGCTCAGCCTGCAGAACTGCTCCCTGACCGAGGCGGGCTGCGGGGTCCTGCCCAGC 306

Qy        740 IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGlu 759
Db        307 ACGCTGCGCTCCCTGCCCACGCTGCGGGAGCTGCATCTCAGCGACAACCCACTGGGGGAC 366

Qy        760 GluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSerLeu 779
Db        367 GCCGGCCTGCGGCTGCTCTGTGAGGGGCTCCTGGACCCCCAGTGCCACCTGGAGAAGCTG 426

Qy        780 ArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThr 799
Db        427 CAGTTGGAGTACTGCCGCCTGACGGCCGCCAGCTGCGAGCCCCTGGCCTCGGTGCTCAGG 486

Qy        800 ThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyVal 819
Db        487 GCCACGCGGGCCTTGAAGGAGCTCACGGTGAGCAACAACGACATCGGCGAGGCCGGCGCC 546
```

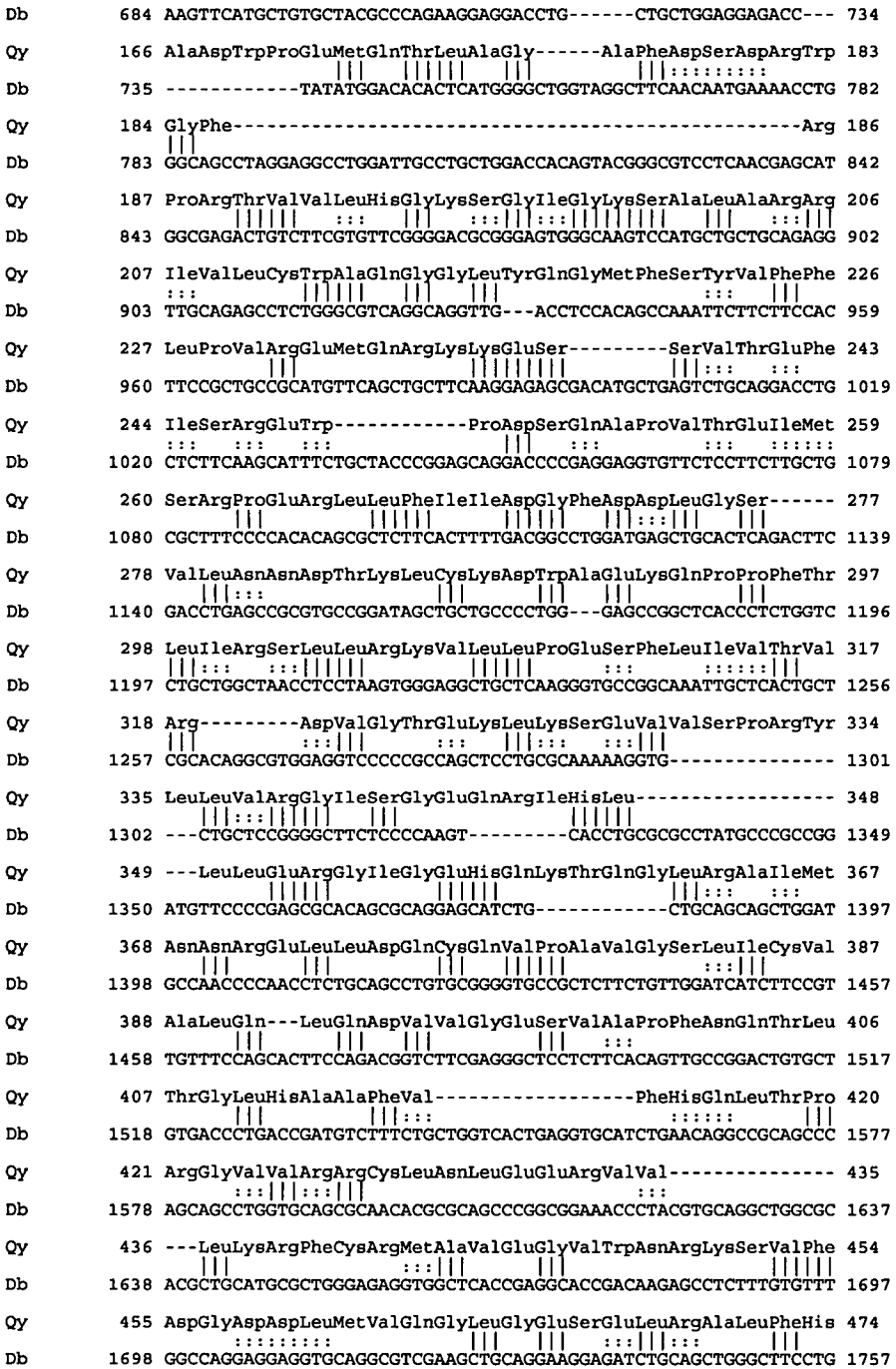
```
Qy        820 MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGlu 839
Db        547 CGGGTGCTGGGCCAGGGTCTGGCAGACTCTGCCTGCCAGCTGGAGACGCTCAGGCTGGAG 606

Qy        840 AspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
Db        607 AACTGCGGTCTCACGCCAGCCAACTGCAAAGACCTGTGCGGAATTGTGGCCTCCCAGGCC 666

Qy        860 SerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeu 879
Db        667 TCGCTGAGGGAGCTTGACCTGGGCAGCAACGGGCTGGGCGACGCGGGCATAGCCGAGCTG 726

Qy        880 CysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899
Db        727 TGCCCCGGGCTCTTGAGCCCCGCCTCCCGCCTCAAGACCCTGTGGCTCTGGGAGTGTGAC 786

Qy        900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThr 919
Db        787 ATCACCGCCAGTGGCTGCAGAGACCTCTGCCGTGTCCTCCAGGCCAAGGAGACCCTGAAG 846

Qy        920 HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGluVal 939
Db        847 GAGCTCAGTCTGGCGGGCAACAAGCTGGGCGACGAGGGCGCCCGGCTGCTGTGCGAGAGC 906

Qy        940 MetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThrAla 959
Db        907 CTGCTGCAGCCCGGCTGCCAGCTGGAGTCCCTGTGGGTGAAGTCCTGCAGCCTCACGGCG 966

Qy        960 AlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAsp 979
Db        967 GCCTGCTGCCAGCACGTCAGCTTGATGCTGACCCAGAACAAGCATCTCCTGGAACTTCAG 1026

Qy        980 LeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGln 999
Db       1027 TTGAGCAGCAACAAGCTGGGTGACTCTGGCATCCAGGAGCTGTGCCAGGCCCTGAGCCAG 1086

Qy       1000 LysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCys 1019
Db       1087 CCGGGCACCACACTGCGGGTGCTCTGTCTTGGGGACTGTGAGGTGACCAACAGCGGCTGC 1146

Qy       1020 GluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGln 1039
Db       1147 AGCAGCCTCGCCTCGCTCCTGCTGGCCAACCGCAGCCTGCGAGAGCTGGACCTGAGCAAC 1206

Qy       1040 AsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSer 1059
Db       1207 AACTGTGTGGGCGACCCGGGCGTCCTGCAGCTGCTGGGGAGCCTGGAGCAGCCGGGCTGC 1266

Qy       1060 AsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleArgLysLeuLeu 1079
Db       1267 GCCCTGGAGCAGCTGGTCCTGTACGACACCTACTGGACGGAGGAGGTGGAGGACCGCCTG 1326

Qy       1080 GluGluValGlnLeuLeuLysPro------ArgValVal 1090
Db       1327 CAGGCCCTGGAGGGGAGCAAGCCCGGCCTGAGGGTCATC 1365

RESULT 10
US-08-910-731-7
; Sequence 7, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1371 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-910-731-7

Alignment Scores:
Pred. No.:                4.18e-55        Length:          1371
Score:                    612.00          Matches:         152
Percent Similarity:       49.26%          Conservative:    81
Best Local Similarity:    32.14%          Mismatches:      214
Query Match:              8.65%           Indels:          26
DB:                       2               Gaps:            5

US-10-066-521-6 (1-1344) x US-08-910-731-7 (1-1371)

Qy        625 AsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIle 644
Db          4 AACCTGGACATT----------------------CATTGCGAGCAGCTGAGCGACGCC 39

Qy        645 ArgValAspValLysGlyIlePheProArgAspGluSerAlaGluAlaCysProValVal 664
Db         40 CGG-------------------------------TGGACAGAGCTCCTGCCGCTGCTC 66

Qy        665 ProLeuTrp-----------MetArgAspLysThrLeuIleGluGluGlnTrpGluAsp 680
Db         67 CAGCAGTATGAGGTGGTCAGGCTCGACGACTGCGGCCTCACGGAGGAGCACTGCAAGGAC 126

Qy        681 PheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIle 700
Db        127 ATCGGTTCTGCCCTCCGGGCCAACCCCTCCCTGACCGAGCTCTGCCTCCGCACCAACGAG 186

Qy        701 LeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCysLysIle 720
Db        187 CTGGGCGATGCCGGCGTGCACCTGGTGCTGCAGGGCCTGCAGAGCCCCACCTGCAAGATC 246

Qy        721 GlnThrLeuMetPheArgAsnAlaGlnIleThr---ProGlyValGlnHisLeuTrpArg 739
Db        247 CAGAAGCTCAGCCTGCAGAACTGCTCCCTGACCGAGGCGGGCTGCGGGGTCCTGCCCAGC 306

Qy        740 IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGlu 759
Db        307 ACGCTGCGCTCCCTGCCCACGCTGCGGGAGCTGCATCTCAGCGACAACCCACTGGGGGAC 366

Qy        760 GluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSerLeu 779
```

```
Db        367 GCCGGCCTGCGGCTGCTCTGTGAGGGGCTCCTGGACCCCCAGTGCCACCTGGAGAAGCTG 426

Qy        780 ArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThr 799
              :::|||:::   |||  ||||||   |||       ::::::   :::|||
Db        427 CAGTTGGAGTACTGCCGCCTGACGGCCGCCAGCTGCGAGCCCCTGGCCTCGGTGCTCAGG 486

Qy        800 ThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyVal 819
                 :::   :::||||||   |||:::::::::   |||   :::   :::   |||
Db        487 GCCACGCGGGCCTTGAAGGAGCTCACGGTGAGCAACAACGACATCGGCGAGGCCGGCGCC 546

Qy        820 MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGlu 839
                 |||           |||       |||   |||   |||:::   |||   ||||||
Db        547 CGGGTGCTGGGCCAGGGTCTGGCCGACTCTGCCTGCCAGCTGGAGACGCTCAGGCTGGAG 606

Qy        840 AspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
              :::||||||:::|||           |||:::   |||         :::   |||
Db        607 AACTGCGGTCTCACGCCAGCCAACTGCAAAGACCTGTGCGGAATTGTGGCCTCCCAGGCC 666

Qy        860 SerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeu 879
              ||||||       |||   |||   :::|||   ||||||:::   |||:::       |||
Db        667 TCGCTGCGGGAGCTGGCCCTGGGCAGCAACAAGCTGGGTGATGTGGGCATGGCGGAGCTG 726

Qy        880 CysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899
              |||     :::     |||           |||:::   |||   :::   :::|||
Db        727 TGCCCAGGGCTGCTCCACCCCAGCTCCAGGCTCAGGACCCTGTGGATCTGGGAGTGTGGC 786

Qy        900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThr 919
              :::         |||||||||   |||         |||                 |||
Db        787 ATCACTGCCAAGGGCTGCGGGGATCTGTGCCGTGTCCTCAGGGCCAAGGAGAGCCTGAAG 846

Qy        920 HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGluVal 939
                 ||||||||||:::   |||   :::   |||   |||   :::||||||||||||
Db        847 GAGCTCAGCCTGGCCGGCAACGAGCTGGGGGATGAGGGTGCCCGACTGCTGTGTGAGACC 906

Qy        940 MetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThrAla 959
              :::   ||||||   |||   |||:::   |||   :::       |||       ||||||
Db        907 CTGCTGGAACCTGGCTGCCAGCTGGAGTCGCTGTGGGTGAAGTCCTGCAGCTTCACAGCC 966

Qy        960 AlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAsp 979
              |||||||||           |||   |||:::::::::::::|||   |||     |||
Db        967 GCCTGCTGCCCCCACTTCAGCTCAGTGCTGGCCCAGAACAGGTTTCTCCTGGAGCTACAG 1026

Qy        980 LeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGln 999
              :::::::::|||   |||   |||   ||||||       ||||||:::|||||   |||
Db       1027 ATAAGCAACAACAGGCTGGAGGATGCGGGCGTGCGGGAGCTGTGCCAGGGCCTGGGCCAG 1086

Qy       1000 LysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCys 1019
              |||||||||           |||   |||       |||   ::::::           |||
Db       1087 CCTGGCTCTGTGCTGCGGGTGCTCTGGTTGGCCGACTGCGATGTGAGTGACAGCAGCTGC 1146

Qy       1020 GluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGln 1039
              :::|||:::       |||       |||       |||       |||:::|||
Db       1147 AGCAGCCTCGCCGCAACCCTGTTGGCCAACCACAGCCTGCGTGAGCTGGACCTCAGCAAC 1206

Qy       1040 AsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSer 1059
              |||               |||:::::::::|||       :::           |||
Db       1207 AACTGCCTGGGGGACGCCGGCATCCTGCAGCTGGTGGAGAGCGTCCGGCAGCCGGGCTGC 1266

Qy       1060 AsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleArgLysLeuLeu 1079
                 |||:::   :::   |||:::       :::       ::::::           |||
Db       1267 CTCCTGGAGCAGCTGGTCCTGTACGACATTTACTGGTCTGAGGAGATGGAGGACCGGCTG 1326

Qy       1080 GluGluValGlnLeuLeuLysPro------ArgValVal 1090
              :::   ::::::       ||||||      ||||||:::
Db       1327 CAGGCCCTGGAGAAGGACAAGCCATCCCTGAGGGTCATC 1365

RESULT 11
US-08-910-731-5
; Sequence 5, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1386 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-910-731-5

Alignment Scores:
Pred. No.:              1.3e-54        Length:          1386
Score:                  607.50         Matches:         144
Percent Similarity:     51.49%         Conservative:    80
Best Local Similarity:  33.10%         Mismatches:      206
Query Match:            8.59%          Indels:          5
DB:                     2              Gaps:            3

US-10-066-521-6 (1-1344) x US-08-910-731-5 (1-1386)

Qy        659 GluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrp 678
              :::   |||   ||||||   |||         |||   |||   :::
Db         82 CAGCAGTGCCAAGTGGTCAGGCTG------GACGACTGTGGCCTCACGGAAGCACGGTGC 135

Qy        679 GluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySer 698
              :::|||       |||   |||       :::|||   |||   :::|||:::|||   |||
Db        136 AAGGACATCAGCTCTGCACTTCGAGTCAACCCTGCACTGGCAGAGCTCAACCTGCGCAGC 195

Qy        699 SerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCys 718
              :::   |||   :::       :::       :::           |||:::   |||:::|||
Db        196 AACGAGCTGGGCGATGTCGGCGTGCATTGCGTGCTCCAGGGCCTGCAGACCCCCTCCTGC 255

Qy        719 LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThr---ProGlyValGlnHisLeu 737
              |||||||||   |||       :::|||       :::|||       |||           |||
Db        256 AAGATCCAGAAGCTGAGCCTCCAGAACTGCTGCCTGACGGGGGCCGGCTGCGGGGTCCTG 315

Qy        738 TrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeu 757
                       :::               |||:::   |||:::|||               |||
Db        316 TCCAGCACACTACGCACCCTGCCCACCCTGCAGGAGCTGCACCTCAGCGACAACCTCTTG 375
```

```
Qy        758 LysGluGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGlu 777
Db        376 GGGGATGCGGGCCTGCAGCTGCTCTGCGAAGGACTCCTGGACCCCCAGTGCCGCCTGGAA 435

Qy        778 SerLeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIle 797
Db        436 AAGCTGCAGCTGGAGTATTGCAGCCTCTCGGCTGCCAGCTGCGAGCCCCTGGCCTCCGTG 495

Qy        798 LeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGln 817
Db        496 CTCAGGGCCAAGCCGGACTTCAAGGAGCTCACGGTTAGCAACAACGACATCAATGAGGCT 555

Qy        818 GlyValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIle 837
Db        556 GGCGTCCGTGTGCTGTGCCAGGGCCTGAAGGACTCCCCCTGCCAGCTGGAGGCGCTCAAG 615

Qy        838 LeuGluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSer 857
Db        616 CTGGAGAGCTGCGGTGTGACATCAGACAACTGCCGGGACCTGTGCGGCATTGTGGCCTCC 675

Qy        858 AsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsn 877
Db        676 AAGGCCTCGCTGCGGGAGCTGGCCCTGGGCAGCAACAAGCTGGGTGATGTGGGCATGGCG 735

Qy        878 LeuLeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGln 897
Db        736 GAGCTGTGCCCAGGGCTGCTCCACCCCAGCTCCAGGCTCAGGACCCTGTGGATCTGGGAG 795

Qy        898 CysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrp 917
Db        796 TGTGGCATCACTGCCAAGGGCTGCGGGGATCTGTGCCGTGTCCTCAGGGCCAAGGAGAGC 855

Qy        918 LeuThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCys 937
Db        856 CTGAAGGAGCTCAGCCTGGCCGGCAACGAGCTGGGGGATGAGGGTGCCCGACTGCTGTGT 915

Qy        938 GluValMetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeu 957
Db        916 GAGACCCTGCTGGAACCTGGCTGCCAGCTGGAGTCGCTGTGGGTGAAGTCCTGCAGCTTC 975

Qy        958 ThrAlaAlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSer 977
Db        976 ACAGCCGCCTGCTGCCCCCACTTCAGCTCAGTGCTGGCCCAGAACAGGTTTCTCCTGGAG 1035

Qy        978 LeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeu 997
Db       1036 CTACAGATAAGCAACAACAGGCTGGAGGATGCGGGCGTGCGGGAGCTGTGCCAGGGCCTG 1095

Qy        998 LysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAsp 1017
Db       1096 GGCCAGCCTGGCTCTGTGCTGCGGGTGCTCTGGTTGGCCGACTGCGATGTGAGTGACAGC 1155

Qy       1018 CysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeu 1037
Db       1156 AGCTGCAGCAGCCTCGCCGCAACCCTGTTGGCCAACCACAGCCTGCGTGAGCTGGACCTC 1215

Qy       1038 ValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysPro 1057
Db       1216 AGCAACAACTGCCTGGGGGACGCCGGCATCCTGCAGCTGGTGGAGAGCGTCCGGCAGCCG 1275

Qy       1058 ThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleArgLys 1077
Db       1276 GGCTGCCTCCTGGAGCAGCTGGTCCTGTACGACATTTACTGGTCTGAGGAGATGGAGGAC 1335

Qy       1078 LeuLeuGluGluValGlnLeuLeuLysPro------ArgValVal 1090
Db       1336 CGGCTGCAGGCCCTGGAGAAGGACAAGCCATCCCTGAGGGTCATC 1380

RESULT 12
US-09-799-451-870
; Sequence 870, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Goodrich, Ryle
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Yamazaki, Victoria
;  APPLICANT:  Chen, Rui-hong
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Yang, Yonghong
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Ghosh, Reena
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. 6783969el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 803
;  CURRENT APPLICATION NUMBER: US/09/799,451
;  CURRENT FILING DATE:  2001-03-05
;  NUMBER OF SEQ ID NOS: 948
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 870
;   LENGTH: 3156
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (478)..(2565)
US-09-799-451-870

Alignment Scores:
Pred. No.:                3.04e-32        Length:          3156
Score:                    406.00          Matches:         286
Percent Similarity:       35.04%          Conservative:    152
Best Local Similarity:    22.88%          Mismatches:      420
Query Match:              5.74%           Indels:          392
DB:                       4               Gaps:            55

US-10-066-521-6 (1-1344) x US-09-799-451-870 (1-3156)

Qy        148 MetThrLysPheAlaGluGluGluAspValArgArgSerPheGluAsnThrAlaAlaAsp 167
Db          1 ATGAGCTACTTCGCCCACCCGGAGGAGCTGGCCCTGGAGCATCAGCCACCCCAGGCCGGG 60

Qy        168 TrpProGluMetGlnThrLeuAlaGlyAlaPheAspSerAspArgTrpGlyPheArgPro 187
Db         61 CTCCCCCCACTG---GCCTTGTCTCAGCTCTTTAACCCGGATGCCTGTGGGCGCCGGGTG 117

Qy        188 ArgThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIle 207
Db        118 CAGACAGTGGTGCTGTATGGGACAGTGGGCACAGGCAAGAGCACGCTGGTGCGCAAGATG 177

Qy        208 ValLeuCysTrpAlaGlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePheLeu 227
Db        178 GTTCTGGACTGGTGTTATGGGCGGCTGCCG-----------GCATTCGAGCTGCTCATC 225

Qy        228 Pro---------------ValArgGluMetGlnArgLysLysGluSerSerValThrGlu 242
Db        226 CCCTTCTCCTGTGAGGACGTGTCATCCGTGGGCCGT---GCCCCAGCCTCCATGTGCCAA 282

Qy        243 PheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMet--------- 259
Db        283 CTTGTGGCCCAGCGCTAC-----------ACGCCCCTGAAGGAGGTTCTGCCCCTGATG 330

Qy        260 ---SerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerVal 278
Db        331 GCTGCTGCTGGGTCCCACCTCCTCTTTGTGCTCCATGGCTTAGAGCAT----------- 378
```



```
Db       2071 CACCTGTCCCTGCTGCACACGGGCCTTGGGGACGAAGGCCTGGAGCTG---------- 2118

Qy        940 MetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThrAla 959

Db       2118 ------------------------------------------------------------ 2118

Qy        960 AlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAsp 979

Db       2119 --------------CTGGCTGCCCAGCTGGACCGCAACCGGCAGCTGCAGGAGCTGAAC 2163

Qy        980 LeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGln 999

Db       2164 GTGGCGTACAACGGTGCTGGTGACACAGCGGCCCTGGCCCTGGCCAGAGCTGCCCGGGAG 2223

Qy       1000 LysAsnSer------------------------------------------------------ 1002

Db       2224 CACCCTTCCCTGGAACTGCTACACCTCTACTTCAATGAGCTGAGCTCAGAGGGCCGCCAG 2283

Qy       1003 ValLeuThrArgLeuGlyLeuLysAlaCysGly--------------------LeuThr 1015

Db       2284 GTCTTGCGAGACTTGGGGGGTGCTGCTGAAGGTGGTGCCCGGGTGGTGGTGTCACTGACA 2343

Qy       1016 SerAspCysCys------GluAlaLeuSerLeuAlaLeuSer---CysAsnArgHisLeu 1032

Db       2344 GAGGGGACGGCGGTGTCAGAATACTGGTCAGTGATCCTCAGTGAAGTCCAGCGGAACCTC 2403

Qy       1033 ThrSerLeuAsn------------------------------LeuValGlnAsnAsnPhe 1042

Db       2404 AATAGCTGGGATCGGGCCCGGGTTCAGCGACACCTTGAGCTCCTACTGCGGGATCTGGAA 2463

Qy       1043 SerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSerAsnLeuGln 1062

Db       2464 GATAGCCGGGGT-----------------GCCACCCTTAATCCTTGGCGCAAGGCCCAG 2505

Qy       1063 IleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleArgLysLeuLeuGluGluVal 1082

Db       2506 CTGCTG--------------CGAGTGGAGGGCGAGGTCAGGGCCCTCCTGGAGCAGCTG 2550

Qy       1083 GlnLeuLeuLysProArgValValIleAspGlySerTrpHisSerPheAspGluAspAsp 1102

Db       2551 ----------------------------GGAAGCTCTGGAAGCTGAGACACTGGCGGC 2580

Qy       1103 ArgHis------------LysIleGlyLeu-ThrPheArgLeuProGluSerArgAlaTr 1118

Db       2581 AGGCACCTAGCTATGTGACCACTGGCCCTAAACCTTTTCCCTC----------------- 2623

Qy       1118 pProCysAlaLeuLeuTrpGlyMetAsnProGluGlnLysLysArgValSerLeuLeuAl 1138

Db       2624 ----TGTGGCCTCCTGGCTTGCACTGCTCCCTCTAGAAAGATTCCTTCAGGTCTGGAGGC 2679

Qy       1138 aGlyAspPhe-LysSerSerThrArgPheAlaLysSerLeuCysLeuAlaThrAlaAsnG 1158

Db       2680 AGAGGAATGGGCATAGCTGAGCCAGTTGCCCTCCTAGGGCATGTTTGACCAGGACTGAGT 2739

Qy       1158 lyGluSerGlnArgValAspAsnValGluGln-SerSerProGlnProMetAlaGlyThr 1177

Db       2740 CTGGAATCTCCAAGTTAAAGATGGTGAATCAATGCTTCGGGCTTGGAGATG--------- 2790

Qy       1178 GluHis--------------------LysGlnAspLysMetLeuSerValGlyTyrSer 1190

Db       2791 GAACATGCCTCCTCTCCATTCAGCTAGAAGGACCAAAGCATGTGGCATTTGGATGGCCAG 2850

Qy       1191 GlyAlaTrp-SerGluThrAlaGluLeuGluGlyLeuGlySerAsnSerAlaAsp----- 1208

Db       2851 AGTGCCCTGAAGCACCACTACCAACCTTGCCTCCCCCTCCTCTCAAAGAGCCTCTGATTG 2910

Qy       1209 ------------------------------HisAspHisGly---------GlyMetAl 1215

Db       2911 TGTCACCAAGGGGCTCACATCTTATGTCTGCCATGCCAGGGGTGTCGCCATCCAGATGTG 2970

Qy       1215 aTrpSerLeuGlyArgGluLeuSerSerArgGlyLeuCysProThrValLeuMetThrTh 1235

Db       2971 TTGGAAGCTT--------------------CCCCTCCTGCCTTATGCTCACCTGTGGAC 3009

Qy       1235 rAlaValCysProGlyHisTrp 1242

Db       3010 ACCGAGGATGCCCTCACATTGG 3031

RESULT 13
US-09-245-281-42
; Sequence 42, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
;  APPLICANT: Bertin, John
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 07334/118001
;  CURRENT APPLICATION NUMBER: US/09/245,281
;  CURRENT FILING DATE: 1999-02-05
;  EARLIER APPLICATION NUMBER: US 09/207,359
;  EARLIER FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 09/099,041
;  EARLIER FILING DATE: 1998-06-17
;  EARLIER APPLICATION NUMBER: US 09/019,942
;  EARLIER FILING DATE: 1998-02-06
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
;   LENGTH: 4141
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (261)...(3119)
US-09-245-281-42

Alignment Scores:
Pred. No.:              3.63e-29        Length:         4141
Score:                  379.50          Matches:        253
Percent Similarity:     37.01%          Conservative:   150
Best Local Similarity:  23.23%          Mismatches:     416
Query Match:            5.36%           Indels:         273
DB:                     3               Gaps:           46

US-10-066-521-6 (1-1344) x US-09-245-281-42 (1-4141)

Qy          6 SerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGluLeuAspLysGluGlu 25

Db        451 AGCCTGACAAGGTCCGAAAGATCCTTGACCTGGTGC----------------------- 486

Qy         26 PheGlnThrPheLysGluLeuLeuLysLysSerSerGluSerThrThrCysSerIle 45

Db        487 ------------AGAGCAAAGGCGAGGAGGTGTCTGAGTTCTTCCTCTACGTGCTGCAG- 533

Qy         46 ProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeuLeuLeuHisGluTyr 65

Db        534 ---------CAGCTGGAGGATGCTTACGTGGAC---CTCAGGCTG--------------- 566

Qy         66 TyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArg 85

Db        567 -----------------TGGCTCTCAGAAATTGGCTTCTCCCCTTCCCAGCTCATTCGG 608

Qy         86 ThrLeuSerGluLysAlaArgAspAspMetLysLysIleSerGlnAlaMetGluGlnGlu 105

Db        609 ACCAAAACTATCGTCAATACTGACCCAGTAAGCAGGTATACCCAACAGCTGCGACACCAA 668

Qy        106 GlyAlaThrAlaAlaGluThrGluGluGlnGluIleSerGlnAlaMetGluGlnGluGly 125

Db        668 ------------------------------------------------------------ 668

Qy        126 AlaThrAlaAlaGluThrGluGluGlnGlyHisGlyGlyAspThrTrpAspTyrLysSer 145

Db        669 ----------------------------CTGGGCCGCGAC--------------TCC 683

Qy        146 HisValMetThrLysPheAlaGluGluGluAspValArgArgSerPheGluAsnThrAla 165
```


Db 684 AAGTTCATGCTGTGCTACGCCCAGAAGGAGGACCTG------CTGCTGGAGGAGACC--- 734
Qy 166 AlaAspTrpProGluMetGlnThrLeuAlaGly------AlaPheAspSerAspArgTrp 183
Db 735 -----------TATATGGACACACTCATGGGGCTGGTAGGCTTCAACAATGAAAACCTG 782
Qy 184 GlyPhe----------Arg 186
Db 783 GGCAGCCTAGGAGGCCTGGATTGCCTGCTGGACCACAGTACGGGCGTCCTCAACGAGCAT 842
Qy 187 ProArgThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArg 206
Db 843 GGCGAGACTGTCTTCGTGTTCGGGGACGCGGGAGTGGGCAAGTCCATGCTGCTGCAGAGG 902
Qy 207 IleValLeuCysTrpAlaGlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePhe 226
Db 903 TTGCAGAGCCTCTGGGCGTCAGGCAGGTTG---ACCTCCACAGCCAAATTCTTCTTCCAC 959
Qy 227 LeuProValArgGluMetGlnArgLysLysGluSer---------SerValThrGluPhe 243
Db 960 TTCCGCTGCCGCATGTTCAGCTGCTTCAAGGAGAGCGACATGCTGAGTCTGCAGGACCTG 1019
Qy 244 IleSerArgGluTrp----------ProAspSerGlnAlaProValThrGluIleMet 259
Db 1020 CTCTTCAAGCATTTCTGCTACCCGGAGCAGGACCCCGAGGAGGTGTTCTCCTTCTTGCTG 1079
Qy 260 SerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySer------ 277
Db 1080 CGCTTTCCCCACACAGCGCTCTTCACTTTGACGGCCTGGATGAGCTGCACTCAGACTTC 1139
Qy 278 ValLeuAsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProProPheThr 297
Db 1140 GACCTGAGCCGCGTGCCGGATAGCTGCTGCCCCTGG---GAGCCGGCTCACCCTCTGGTC 1196
Qy 298 LeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrVal 317
Db 1197 CTGCTGGCTAACCTCCTAAGTGGGAGGCTGCTCAAGGGTGCCGGCAAATTGCTCACTGCT 1256
Qy 318 Arg---------AspValGlyThrGluLysLeuLysSerGluValValSerProArgTyr 334
Db 1257 CGCACAGGCGTGGAGGTCCCCCGCCAGCTCCTGCGCAAAAAGGTG-------------- 1301
Qy 335 LeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeu---------------- 348
Db 1302 ---CTGCTCCGGGGCTTCTCCCCAAGT---------CACCTGCGCGCCTATGCCCGCCGG 1349
Qy 349 ---LeuLeuGluArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMet 367
Db 1350 ATGTTCCCCGAGCGCACAGCGCAGGAGCATCTG-----------CTGCAGCAGCTGGAT 1397
Qy 368 AsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysVal 387
Db 1398 GCCAACCCCAACCTCTGCAGCCTGTGCGGGGTGCCGCTCTTCTGTTGGATCATCTTCCGT 1457
Qy 388 AlaLeuGln---LeuGlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeu 406
Db 1458 TGTTTCCAGCACTTCCAGACGGTCTTCGAGGGCTCCTCTTCACAGTTGCCGGACTGTGCT 1517
Qy 407 ThrGlyLeuHisAlaAlaPheVal----------PheHisGlnLeuThrPro 420
Db 1518 GTGACCCTGACCGATGTCTTTCTGCTGGTCACTGAGGTGCATCTGAACAGGCCGCAGCCC 1577
Qy 421 ArgGlyValValArgArgCysLeuAsnLeuGluGluArgValVal---------- 435
Db 1578 AGCAGCCTGGTGCAGCGCAACACGCGCAGCCCGGCGGAAACCCTACGTGCAGGCTGGCGC 1637
Qy 436 ---LeuLysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerValPhe 454
Db 1638 ACGCTGCATGCGCTGGGAGAGGTGGCTCACCGAGGCACCGACAAGAGCCTCTTTGTGTTT 1697
Qy 455 AspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHis 474
Db 1698 GGCCAGGAGGAGGTGCAGGCGTCGAAGCTGCAGGAAGGAGATCTGCAGCTGGGCTTCCTG 1757
Qy 475 MetAsnIleLeuLeuProAspSerHisCysGlu------GluTyrTyrThrPhePheHis 492
Db 1758 CGG------GCTTTGCCCGATGTGGGCCCTGAGCAGGGCCAGTCTTACGAATTTTTCCAC 1811
Qy 493 LeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluIleGlu 512
Db 1812 CTTACGCTCCAGGCCTTCTTCACCGCCTTCTTCCTGGTAGCAGATGACAAAGTGAGCACC 1871
Qy 513 ProAlaLeuCysProLeuTyrValGluLysThrLysArgSerMetGluLeuLysGlnAla 532
Db 1872 CGGGAGTTGCTGAGGTTCTTTCGAGAATGGACGTCTCCTGGA---GAGGCAACAAGCTCG 1928
Qy 533 GlyPheHisIle---------- 536
Db 1929 TCCTGCCATTCTTCCTTCTTCTCCTTCCAGTGCCTGGGCGGCAGAAGCCGGTTGGGCCCT 1988
Qy 537 ----------HisSerLeuTrpMetLysArgPheLeuPheGlyLeuVal 549
Db 1989 GATCCTTTCAGGAACAAAGATCACTTCCAGTTCACCAACCTCTTCGTGTGCGGGCTACTG 2048
Qy 550 SerGluAspValArgArgProLeuGluValLeuLeuGlyCysProValProLeuGlyVal 569
Db 2049 GCCAAAGCCCGACAGAAACTCCTTCGGCAGCTG----------GTGCCCAAGGCTATC 2096
Qy 570 ---------LysGlnLysLeuLeuHisTrpVal----------SerLeu 579
Db 2097 CTGAGGAGGAAGCGCAAGGCCCTG---TGGGCTCACCTGTTTGCTAGCCTGCGCTCCTAC 2153
Qy 580 LeuGlyGlnGlnProAsnAlaThrThrProGly----------Asp 591
Db 2154 TTGAAGAGCCTACCTCGGGTCCAGTCTGGAGGCTTTAACCAGGTGCATGCCATGCCCACA 2213
Qy 592 ThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAla 611
Db 2214 TTCCTGTGGATGCTGCGCTGCATCTATGAGACGCAGAGCCAGAAGGTGGGGCGCCTCGCC 2273
Qy 612 LeuAsnSerPheGlnGluValTrpLeuProIle----------AsnGlnAsnLeuAsp 627
Db 2274 GCCAGGGGCATCAGTGCGGACTACCTCAAGCTGGCCTTTTGCAACGCTTGCTCTGCGGAC 2333
Qy 628 LeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArgValAsp 647
Db 2334 TGCAGCGCCCTGTCCTTCGTCCTGCATCAC------TTCCACAGGCAGCTGGCCCTAGAC 2387
Qy 648 ValLysGlyIlePheProArgAspGluSerAlaGluAlaCysProValValProLeuTrp 667
Db 2388 CTGGACAACAACAACCTCAATGACTATGGCGTGCAG------GAGCTGCAGCCTTGCTTT 2441
Qy 668 MetArgAspLysThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGlyThr 687
Db 2442 AGCCGT---------- 2447
Qy 688 HisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLys 707
Db 2448 ---------CTCACGGTTATCAGACTCAGCGTCAACCAGATCACCGACACGGGGGTGAAG 2498
Qy 708 ThrLeuCysAlaLysLeuArgHisProThrCysLysIleGlnThrLeuMet---PheArg 726
Db 2499 GTGCTATGTGAGGAACTG------ACCAAGTATAAGATCGTGACGTTCCTGGGTTTATAC 2552
Qy 727 AsnAlaGlnIleThrPro---GlyValGlnHisLeuTrpArgIleValMetAlaAsnArg 745
Db 2553 AACAACCAGATAACTGATATCGGAGCCAGGTATGTGGCCCAAATCCTGGATGAATGCAGA 2612
Qy 746 AsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGluGluAspValArgMetAla 765
Db 2613 GGCCTCAAGCACCTTAAACTAGGGAAAAACAGAATAACAAGTGAGGGCGGGAAGTGTGTG 2672
Qy 766 CysGluAlaLeuLysHisProLysCysLeuLeuGluSerLeuArgLeuAspCysCysGly 785
Db 2673 GCTTTGGCTGTGAAGAAC---------- 2690

```
Qy       786 LeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLys 805
                                                        |||   |||:::
Db      2691 ----------------------------------------------AGCACCTCCATCGTT 2705

Qy       806 SerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAla 825
               :::   :::   ||||||::::::   |||:::|||             :::::|||
Db      2706 GATGTTGGGATGTGGGGTAATCAGATTGGAGACGAAGGGGCAAAGGCCTTCGCAGAGGCA 2765

Qy       826 LeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAla 845
               |||:::        :::|||      |||   |||        ||||||:::
Db      2766 TTGAAG---GACCACCCCAGCCTGACCACTCTCAGTCTTGCATTCAATGGCATCTCTCCG 2822

Qy       846 ThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCys 865
               |||   :::||||||||||   ||||||      |||   :::||||||   :::
Db      2823 GAGGGAGGGAAGAGCCTTGCGCAGGCCCTGAAGCAGAACACCACACTGACAGTAATCTGG 2882

Qy       866 LeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeu 885
               |||:::   |||   |||   :::|||                  :::|||:::
Db      2883 CTGACCAAAAATGAACTTAATGATGAGTCTGCAGAGTGCTTCGCTGAGATGCTGAGAGTG 2942

Qy       886 ProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCys 905
               :::   :::|||:::   |||   |||   |||      :::          |||
Db      2943 ---AACCAGACGCTACGGCATTTATGGCTGATCCAGAATCGCATCACAGCCAAGGGGACA 2999

Qy       906 GlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMet 925
               ||||||   ||||||      |||:::   :::|||   :::   |||:::
Db      3000 GCGCAGCTGGCGAGGGCACTGCAGAAGAACACAGCCATAACAGAGATTTGTCTCAATGGA 3059

Qy       926 AsnProValGlu--------------------AspAsnGlyValLysLeuLeuCysGlu 938
               |||   ::::::                        :::|||      :::::::::|||
Db      3060 AACTTGATTAAGCCCGAGGAGGCCAAAGTCTTCGAGAATGAGAAGAGAATCATCTGCTT- 3118

Qy       939 ValMetArgGluProSerCysHisLeuGlnAspLeu------GluLeuValLysCysHis 956
               :::         |||          |||||||||          |||:::      |||
Db      3119 CTGACGGACGCTCCTGGG---------CAGGATCTTTGTCCTAGGTTGCTCCTCAGTCAC 3169

Qy       957 LeuThrAlaAlaCys-----------------------CysGluSerLeuSerCysVal 968
               ||||||   |||                        |||   :::   |||   |||
Db      3170 AG-ACAGCACTGTGCAGTCAGCAGGGTAGCAGGATGCTGTGCAGCGCCTGCAGCAAGGTG 3228

Qy       969 IleSerArgSerArgHisLeuLysSer 977
               ||||||  ||||||  |||
Db      3229 CCTGTCAGGAGCCCACACCTCCACAGT 3255
```

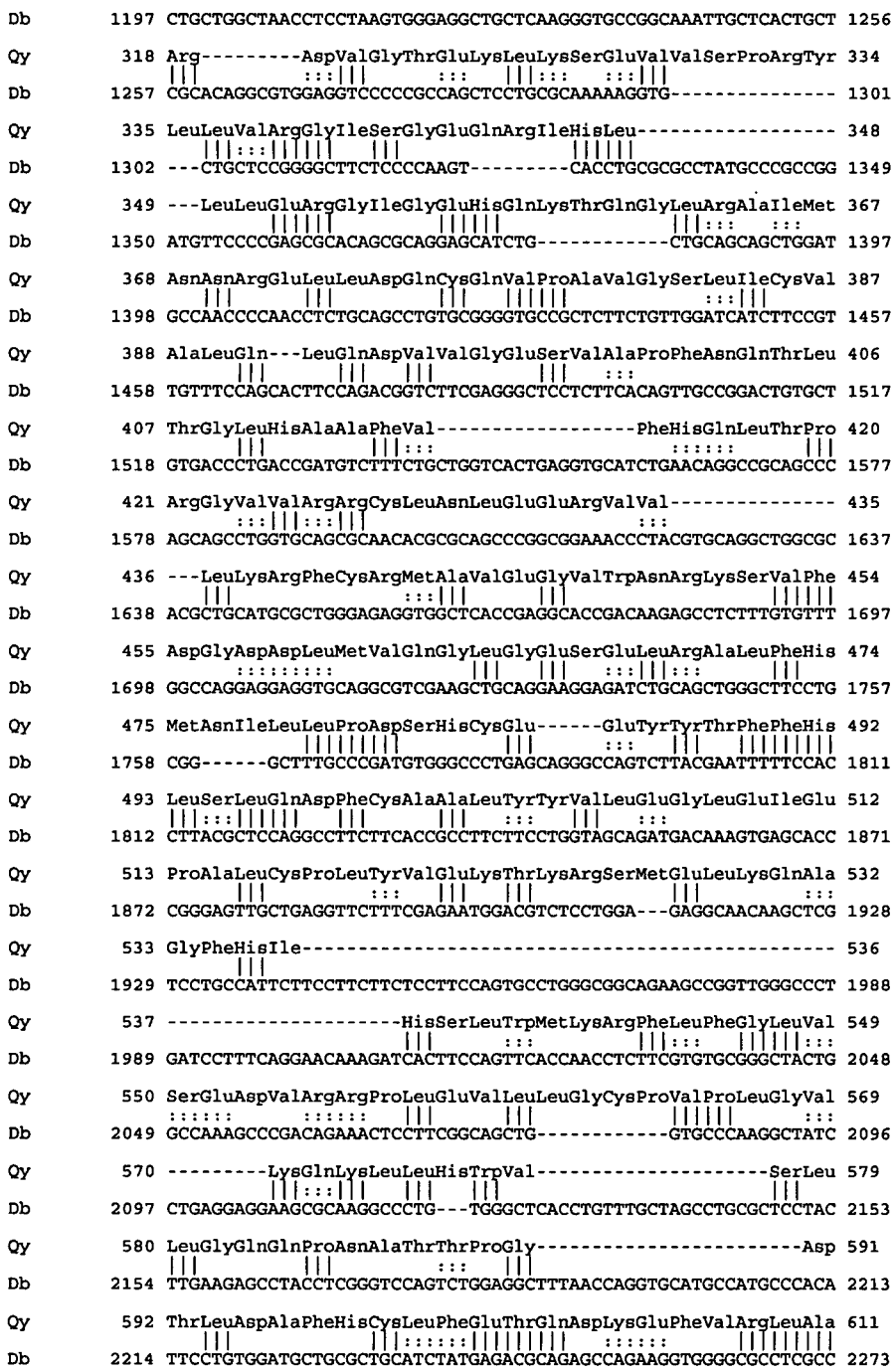
RESULT 14
US-09-207-359B-42
; Sequence 42, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 4141
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (261)...(3119)
US-09-207-359B-42

Alignment Scores:

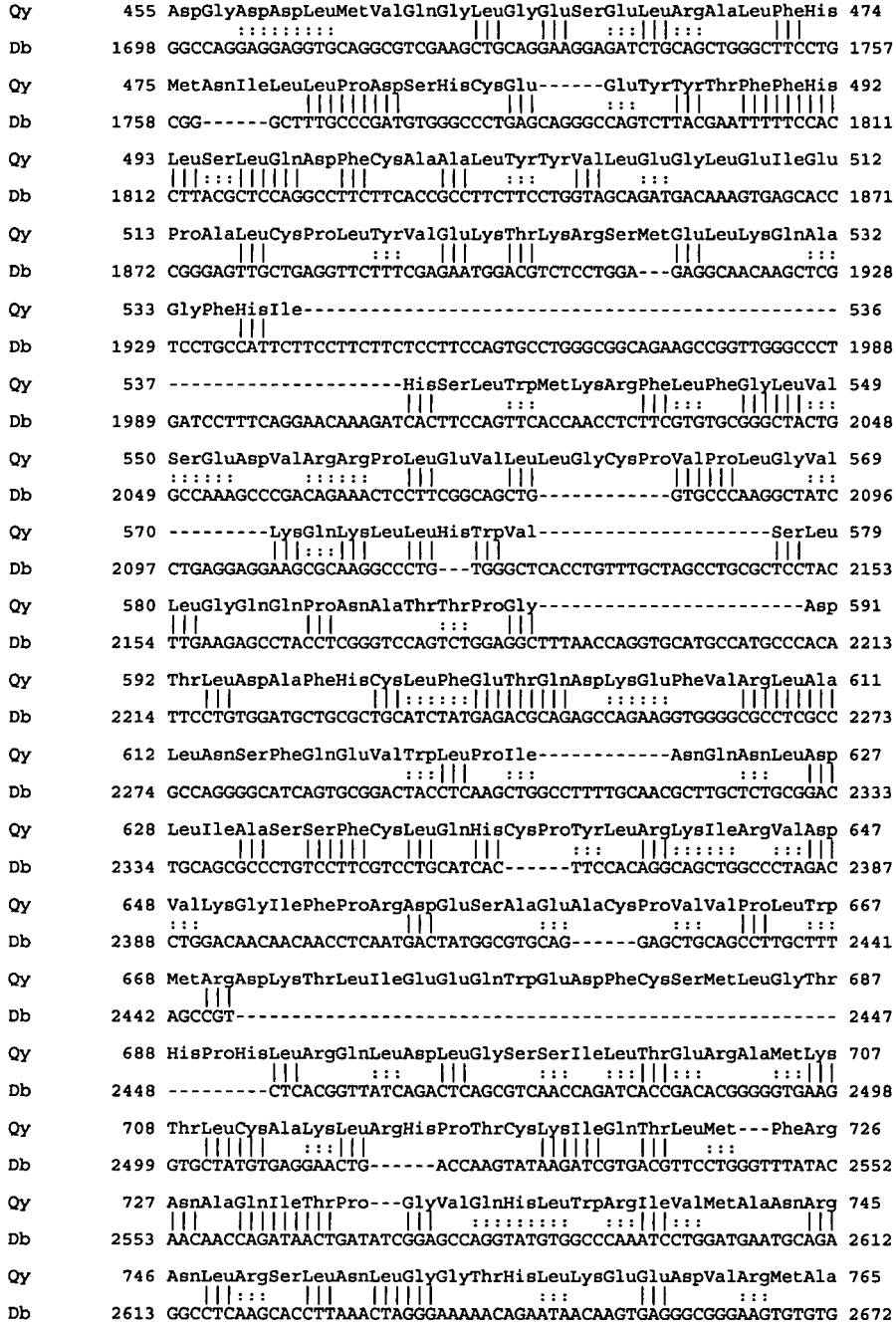
Pred. No.:	3.63e-29	Length:	4141
Score:	379.50	Matches:	253
Percent Similarity:	37.01%	Conservative:	150
Best Local Similarity:	23.23%	Mismatches:	416
Query Match:	5.36%	Indels:	273
DB:	3	Gaps:	46

US-10-066-521-6 (1-1344) x US-09-207-359B-42 (1-4141)

```
Qy         6 SerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGluLeuAspLysGluGlu 25
             |||||||||   |||         |||   ||||||
Db       451 AGCCTGACAAGGTCCGAAAGATCCTTGACCTGGTGC------------------------ 486

Qy        26 PheGlnThrPheLysGluLeuLeuLysLysLysSerSerGluSerThrThrCysSerIle 45
                     :::         ::::::         |||   |||:::||||||
Db       487 -----------AGAGCAAAGGCGAGGAGGTGTCTGAGTTCTTCCTCTACGTGCTGCAG- 533

Qy        46 ProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeuLeuLeuHisGluTyr 65
                    ::::::|||:::|||   |||:::   |||   |||
Db       534 ---------CAGCTGGAGGATGCTTACGTGGAC---CTCAGGCTG-------------- 566

Qy        66 TyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArg 85
                           |||   :::   |||             :::      :::|||
Db       567 -----------------TGGCTCTCAGAAATTGGCTTCTCCCCTTCCCAGCTCATTCGG 608

Qy        86 ThrLeuSerGluLysAlaArgAspAspMetLysLysIleSerGlnAlaMetGluGlnGlu 105
             |||   :::              |||   :::   :::   :::|||   :::      :::
Db       609 ACCAAAACTATCGTCAATACTGACCCAGTAAGCAGGTATACCCAACAGCTGCGACACCAA 668

Qy       106 GlyAlaThrAlaAlaGluThrGluGluGlnGluIleSerGlnAlaMetGluGlnGluGly 125

Db       668 ------------------------------------------------------------ 668

Qy       126 AlaThrAlaAlaGluThrGluGluGlnGlyHisGlyGlyAspThrTrpAspTyrLysSer 145
                                                  |||   |||              |||
Db       669 ----------------------------CTGGGCCGCGAC--------------TCC 683

Qy       146 HisValMetThrLysPheAlaGluGluGluAspValArgArgSerPheGluAsnThrAla 165
                |||      :::|||::::::||||||:::          |||   |||
Db       684 AAGTTCATGCTGTGCTACGCCCAGAAGGAGGACCTG------CTGCTGGAGGAGACC--- 734

Qy       166 AlaAspTrpProGluMetGlnThrLeuAlaGly------AlaPheAspSerAspArgTrp 183
                         |||   ||||||   |||          |||:::::::::
Db       735 -----------TATATGGACACACTCATGGGGCTGGTAGGCTTCAACAATGAAAACCTG 782

Qy       184 GlyPhe-------------------------------------------------Arg 186
             |||
Db       783 GGCAGCCTAGGAGGCCTGGATTGCCTGCTGGACCACAGTACGGGCGTCCTCAACGAGCAT 842

Qy       187 ProArgThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArg 206
                |||||   :::   |||   :::|||:::|||||||||   |||   :::|||
Db       843 GGCGAGACTGTCTTCGTGTTCGGGGACGCGGGAGTGGGCAAGTCCATGCTGCTGCAGAGG 902

Qy       207 IleValLeuCysTrpAlaGlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePhe 226
                :::         ||||||   |||   |||                :::   |||
Db       903 TTGCAGAGCCTCTGGGCGTCAGGCAGGTTG---ACCTCCACAGCCAAATTCTTCTTCCAC 959

Qy       227 LeuProValArgGluMetGlnArgLysLysGluSer---------SerValThrGluPhe 243
                   |||                |||||||||         |||:::   :::
Db       960 TTCCGCTGCCGCATGTTCAGCTGCTTCAAGGAGAGCGACATGCTGAGTCTGCAGGACCTG 1019

Qy       244 IleSerArgGluTrp------------ProAspSerGlnAlaProValThrGluIleMet 259
                :::   :::   :::                 |||   :::          :::   ::::::
Db      1020 CTCTTCAAGCATTTCTGCTACCCGGAGCAGGACCCCGAGGAGGTGTTCTCCTTCTTGCTG 1079

Qy       260 SerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySer------ 277
                   |||          ||||||   ||||||   |||:::|||   |||
Db      1080 CGCTTTCCCCACACAGCGCTCTTCACTTTTGACGGCCTGGATGAGCTGCACTCAGACTTC 1139

Qy       278 ValLeuAsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProProPheThr 297
                |||:::         |||   |||   |||   |||          |||
Db      1140 GACCTGAGCCGCGTGCCGGATAGCTGCTGCCCCTGG---GAGCCGGCTCACCCTCTGGTC 1196

Qy       298 LeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrVal 317
                |||:::   :::||||||         ||||||      :::      ::::::|||
```


Db 1197 CTGCTGGCTAACCTCCTAAGTGGGAGGCTGCTCAAGGGTGCCGGCAAATTGCTCACTGCT 1256
Qy 318 Arg---------AspValGlyThrGluLysLeuLysSerGluValValSerProArgTyr 334
Db 1257 CGCACAGGCGTGGAGGTCCCCCGCCAGCTCCTGCGCAAAAAGGTG---------- 1301
Qy 335 LeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeu---------- 348
Db 1302 ---CTGCTCCGGGGCTTCTCCCCAAGT---------CACCTGCGCGCCTATGCCCGCCGG 1349
Qy 349 ---LeuLeuGluArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMet 367
Db 1350 ATGTTCCCCGAGCGCACAGCGCAGGAGCATCTG-----------CTGCAGCAGCTGGAT 1397
Qy 368 AsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysVal 387
Db 1398 GCCAACCCCAACCTCTGCAGCCTGTGCGGGGTGCCGCTCTTCTGTTGGATCATCTTCCGT 1457
Qy 388 AlaLeuGln---LeuGlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeu 406
Db 1458 TGTTTCCAGCACTTCCAGACGGTCTTCGAGGGCTCCTCTTCACAGTTGCCGGACTGTGCT 1517
Qy 407 ThrGlyLeuHisAlaAlaPheVal----------PheHisGlnLeuThrPro 420
Db 1518 GTGACCCTGACCGATGTCTTTCTGCTGGTCACTGAGGTGCATCTGAACAGGCCGCAGCCC 1577
Qy 421 ArgGlyValValArgArgCysLeuAsnLeuGluGluArgValVal---------- 435
Db 1578 AGCAGCCTGGTGCAGCGCAACACGCGCAGCCCGGCGGAAACCCTACGTGCAGGCTGGCGC 1637
Qy 436 ---LeuLysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerValPhe 454
Db 1638 ACGCTGCATGCGCTGGGAGAGGTGGCTCACCGAGGCACCGACAAGAGCCTCTTTGTGTTT 1697
Qy 455 AspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHis 474
Db 1698 GGCCAGGAGGAGGTGCAGGCGTCGAAGCTGCAGGAAGGAGATCTGCAGCTGGGCTTCCTG 1757
Qy 475 MetAsnIleLeuLeuProAspSerHisCysGlu------GluTyrTyrThrPhePheHis 492
Db 1758 CGG------GCTTTGCCCGATGTGGGCCCTGAGCAGGGCCAGTCTTACGAATTTTTCCAC 1811
Qy 493 LeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluIleGlu 512
Db 1812 CTTACGCTCCAGGCCTTCTTCACCGCCTTCTTCCTGGTAGCAGATGACAAAGTGAGCACC 1871
Qy 513 ProAlaLeuCysProLeuTyrValGluLysThrLysArgSerMetGluLeuLysGlnAla 532
Db 1872 CGGGAGTTGCTGAGGTTCTTTCGAGAATGGACGTCTCCTGGA---GAGGCAACAAGCTCG 1928
Qy 533 GlyPheHisIle---------- 536
Db 1929 TCCTGCCATTCTTCCTTCTTCTCCTTCCAGTGCCTGGGCGGCAGAAGCCGGTTGGGCCCT 1988
Qy 537 ----------HisSerLeuTrpMetLysArgPheLeuPheGlyLeuVal 549
Db 1989 GATCCTTTCAGGAACAAAGATCACTTCCAGTTCACCAACCTCTTCGTGTGCGGGCTACTG 2048
Qy 550 SerGluAspValArgArgProLeuGluValLeuLeuGlyCysProValProLeuGlyVal 569
Db 2049 GCCAAAGCCCGACAGAAACTCCTTCGGCAGCTG-----------GTGCCCAAGGCTATC 2096
Qy 570 ---------LysGlnLysLeuLeuHisTrpVal----------SerLeu 579
Db 2097 CTGAGGAGGAAGCGCAAGGCCCTG---TGGGCTCACCTGTTTGCTAGCCTGCGCTCCTAC 2153
Qy 580 LeuGlyGlnGlnProAsnAlaThrThrProGly----------Asp 591
Db 2154 TTGAAGAGCCTACCTCGGGTCCAGTCTGGAGGCTTTAACCAGGTGCATGCCATGCCCACA 2213
Qy 592 ThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAla 611
Db 2214 TTCCTGTGGATGCTGCGCTGCATCTATGAGACGCAGAGCCAGAAGGTGGGGCGCCTCGCC 2273
Qy 612 LeuAsnSerPheGlnGluValTrpLeuProIle----------AsnGlnAsnLeuAsp 627
Db 2274 GCCAGGGGCATCAGTGCGGACTACCTCAAGCTGGCCTTTTGCAACGCTTGCTCTGCGGAC 2333
Qy 628 LeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArgValAsp 647
Db 2334 TGCAGCGCCCTGTCCTTCGTCCTGCATCAC------TTCCACAGGCAGCTGGCCCTAGAC 2387
Qy 648 ValLysGlyIleProArgAspGluSerAlaGluAlaCysProValValProLeuTrp 667
Db 2388 CTGGACAACAACAACCTCAATGACTATGGCGTGCAG------GAGCTGCAGCCTTGCTTT 2441
Qy 668 MetArgAspLysThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGlyThr 687
Db 2442 AGCCGT---------- 2447
Qy 688 HisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLys 707
Db 2448 ---------CTCACGGTTATCAGACTCAGCGTCAACCAGATCACCGACACGGGGGTGAAG 2498
Qy 708 ThrLeuCysAlaLysLeuArgHisProThrCysLysIleGlnThrLeuMet---PheArg 726
Db 2499 GTGCTATGTGAGGAACTG------ACCAAGTATAAGATCGTGACGTTCCTGGGTTTATAC 2552
Qy 727 AsnAlaGlnIleThrPro---GlyValGlnHisLeuTrpArgIleValMetAlaAsnArg 745
Db 2553 AACAACCAGATAACTGATATCGGAGCCAGGTATGTGGCCCAAATCCTGGATGAATGCAGA 2612
Qy 746 AsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGluGluAspValArgMetAla 765
Db 2613 GGCCTCAAGCACCTTAAACTAGGGAAAAACAGAATAACAAGTGAGGGCGGGAAGTGTGTG 2672
Qy 766 CysGluAlaLeuLysHisProLysCysLeuLeuGluSerLeuArgLeuAspCysCysGly 785
Db 2673 GCTTTGGCTGTGAAGAAC---------- 2690
Qy 786 LeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLys 805
Db 2691 ----------AGCACCTCCATCGTT 2705
Qy 806 SerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAla 825
Db 2706 GATGTTGGGATGTGGGGTAATCAGATTGGAGACGAAGGGGCAAAGGCCTTCGCAGAGGCA 2765
Qy 826 LeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAla 845
Db 2766 TTGAAG---GACCACCCCAGCCTGACCACTCTCAGTCTTGCATTCAATGGCATCTCTCCG 2822
Qy 846 ThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCys 865
Db 2823 GAGGGAGGGAAGAGCCTTGCGCAGGCCCTGAAGCAGAACACCACACTGACAGTAATCTGG 2882
Qy 866 LeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeu 885
Db 2883 CTGACCAAAAATGAACTTAATGATGAGTCTGCAGAGTGCTTCGCTGAGATGCTGAGAGTG 2942
Qy 886 ProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCys 905
Db 2943 ---AACCAGACGCTACGGCATTTATGGCTGATCCAGAATCGCATCACAGCCAAGGGGACA 2999
Qy 906 GlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMet 925
Db 3000 GCGCAGCTGGCGAGGGCACTGCAGAAGAACACAGCCATAACAGAGATTTGTCTCAATGGA 3059
Qy 926 AsnProValGlu----------AspAsnGlyValLysLeuLeuCysGlu 938
Db 3060 AACTTGATTAAGCCCGAGGAGGCCAAAGTCTTCGAGAATGAGAAGAGAATCATCTGCTT- 3118
Qy 939 ValMetArgGluProSerCysHisLeuGlnAspLeu------GluLeuValLysCysHis 956
Db 3119 CTGACGGACGCTCCTGGG---------CAGGATCTTTGTCCTAGGTTGCTCCTCAGTCAC 3169

```
Qy        957 LeuThrAlaAlaCys----------------------CysGluSerLeuSerCysVal 968
              ||||||   |||                     |||   :::   |||   |||
Db       3170 AG-ACAGCACTGTGCAGTCAGCAGGGTAGCAGGATGCTGTGCAGCGCCTGCAGCAAGGTG 3228

Qy        969 IleSerArgSerArgHisLeuLysSer 977
              ||||||   ||||||   |||
Db       3229 CCTGTCAGGAGCCCACACCTCCACAGT 3255

RESULT 15
US-09-340-620A-42
; Sequence 42, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
;  APPLICANT: Bertin, John
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
;  FILE REFERENCE: 07334-124001
;  CURRENT APPLICATION NUMBER: US/09/340,620A
;  CURRENT FILING DATE:  1999-06-28
;  PRIOR APPLICATION NUMBER: US 09/245,281
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: US 09/207,359
;  PRIOR FILING DATE: 1998-12-08
;  PRIOR APPLICATION NUMBER: US 09/099,041
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: US 09/019,942
;  PRIOR FILING DATE: 1998-02-06
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
;   LENGTH: 4141
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (261)...(3119)
US-09-340-620A-42

Alignment Scores:
Pred. No.:              3.63e-29      Length:         4141
Score:                  379.50        Matches:        253
Percent Similarity:     37.01%        Conservative:   150
Best Local Similarity:  23.23%        Mismatches:     416
Query Match:            5.36%         Indels:         273
DB:                     4             Gaps:           46

US-10-066-521-6 (1-1344) x US-09-340-620A-42 (1-4141)

Qy          6 SerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGluLeuAspLysGluGlu 25
              |||||||||   |||         |||   ||||||
Db        451 AGCCTGACAAGGTCCGAAAGATCCTTGACCTGGTGC---------------------- 486

Qy         26 PheGlnThrPheLysGluLeuLeuLysLysLysSerSerGluSerThrThrCysSerIle 45
                        :::         ::::::      |||   |||:::||||||
Db        487 -----------AGAGCAAAGGCGAGGAGGTGTCTGAGTTCTTCCTCTACGTGCTGCAG- 533

Qy         46 ProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeuLeuLeuHisGluTyr 65
                  ::::::|||:::|||   |||:::   |||   |||
Db        534 ---------CAGCTGGAGGATGCTTACGTGGAC---CTCAGGCTG-------------- 566

Qy         66 TyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArg 85
                           |||   :::   |||             :::      :::|||
Db        567 -----------------TGGCTCTCAGAAATTGGCTTCTCCCCTTCCCAGCTCATTCGG 608

Qy         86 ThrLeuSerGluLysAlaArgAspAspMetLysLysIleSerGlnAlaMetGluGlnGlu 105
              |||   :::             |||   :::   :::   :::|||   :::      :::
Db        609 ACCAAAACTATCGTCAATACTGACCCAGTAAGCAGGTATACCCAACAGCTGCGACACCAA 668

Qy        106 GlyAlaThrAlaAlaGluThrGluGluGlnGluIleSerGlnAlaMetGluGlnGluGly 125

Db        668 ------------------------------------------------------------ 668

Qy        126 AlaThrAlaAlaGluThrGluGluGlnGlyHisGlyGlyAspThrTrpAspTyrLysSer 145
                                              |||   |||                |||

Db        669 ----------------------------CTGGGCCGCGAC--------------TCC 683

Qy        146 HisValMetThrLysPheAlaGluGluGluAspValArgArgSerPheGluAsnThrAla 165
                  |||       :::|||::::::||||||:::                |||   |||
Db        684 AAGTTCATGCTGTGCTACGCCCAGAAGGAGGACCTG------CTGCTGGAGGAGACC--- 734

Qy        166 AlaAspTrpProGluMetGlnThrLeuAlaGly------AlaPheAspSerAspArgTrp 183
                           |||   ||||||   |||          |||:::::::::
Db        735 -----------TATATGGACACACTCATGGGGCTGGTAGGCTTCAACAATGAAAACCTG 782

Qy        184 GlyPhe-------------------------------------------------Arg 186
              |||
Db        783 GGCAGCCTAGGAGGCCTGGATTGCCTGCTGGACCACAGTACGGGCGTCCTCAACGAGCAT 842

Qy        187 ProArgThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArg 206
                  ||||||   :::   |||   :::|||:::|||||||||   |||   ::|||
Db        843 GGCGAGACTGTCTTCGTGTTCGGGGACGCGGGAGTGGGCAAGTCCATGCTGCTGCAGAGG 902

Qy        207 IleValLeuCysTrpAlaGlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePhe 226
                  :::         ||||||   |||   |||                  :::   |||
Db        903 TTGCAGAGCCTCTGGGCGTCAGGCAGGTTG---ACCTCCACAGCCAAATTCTTCTTCCAC 959

Qy        227 LeuProValArgGluMetGlnArgLysLysGluSer---------SerValThrGluPhe 243
                  |||                 |||||||||         |||:::   :::
Db        960 TTCCGCTGCCGCATGTTCAGCTGCTTCAAGGAGAGCGACATGCTGAGTCTGCAGGACCTG 1019

Qy        244 IleSerArgGluTrp-----------ProAspSerGlnAlaProValThrGluIleMet 259
                  :::   :::   :::                |||   :::         :::   ::::::
Db       1020 CTCTTCAAGCATTTCTGCTACCCGGAGCAGGACCCCGAGGAGGTGTTCTCCTTCTTGCTG 1079

Qy        260 SerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySer------ 277
                  |||         ||||||   ||||||   |||:::|||   |||
Db       1080 CGCTTTCCCCACACAGCGCTCTTCACTTTTGACGGCCTGGATGAGCTGCACTCAGACTTC 1139

Qy        278 ValLeuAsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProProPheThr 297
                  |||:::               |||   |||   |||   |||
Db       1140 GACCTGAGCCGCGTGCCGGATAGCTGCTGCCCCTGG---GAGCCGGCTCACCCTCTGGTC 1196

Qy        298 LeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrVal 317
                  |||:::   :::||||||         ||||||      :::      ::::::|||
Db       1197 CTGCTGGCTAACCTCCTAAGTGGGAGGCTGCTCAAGGGTGCCGGCAAATTGCTCACTGCT 1256

Qy        318 Arg---------AspValGlyThrGluLysLeuLysSerGluValValSerProArgTyr 334
                  |||         :::|||      :::   |||:::   :::|||
Db       1257 CGCACAGGCGTGGAGGTCCCCCGCCAGCTCCTGCGCAAAAAGGTG--------------- 1301

Qy        335 LeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeu------------------ 348
                  |||:::||||||   |||                |||||
Db       1302 ---CTGCTCCGGGGCTTCTCCCCAAGT---------CACCTGCGCGCCTATGCCCGCCGG 1349

Qy        349 ---LeuLeuGluArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMet 367
                     ||||||         ||||||               |||:::   :::
Db       1350 ATGTTCCCCGAGCGCACAGCGCAGGAGCATCTG-----------CTGCAGCAGCTGGAT 1397

Qy        368 AsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysVal 387
                  |||       |||       |||   ||||||            :::|||
Db       1398 GCCAACCCCAACCTCTGCAGCCTGTGCGGGGTGCCGCTCTTCTGTTGGATCATCTTCCGT 1457

Qy        388 AlaLeuGln---LeuGlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeu 406
                  |||   |||   |||         |||   :::
Db       1458 TGTTTCCAGCACTTCCAGACGGTCTTCGAGGGCTCCTCTTCACAGTTGCCGGACTGTGCT 1517

Qy        407 ThrGlyLeuHisAlaAlaPheVal-----------------PheHisGlnLeuThrPro 420
                  |||         |||:::                   ::::::      |||
Db       1518 GTGACCCTGACCGATGTCTTTCTGCTGGTCACTGAGGTGCATCTGAACAGGCCGCAGCCC 1577

Qy        421 ArgGlyValValArgArgCysLeuAsnLeuGluGluArgValVal--------------- 435
                  :::|||:::|||                     :::
Db       1578 AGCAGCCTGGTGCAGCGCAACACGCGCAGCCCGGCGGAAACCCTACGTGCAGGCTGGCGC 1637

Qy        436 ---LeuLysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerValPhe 454
                     |||         :::|||   |||                  ||||||
Db       1638 ACGCTGCATGCGCTGGGAGAGGTGGCTCACCGAGGCACCGACAAGAGCCTCTTTGTGTTT 1697
```



Search completed: February 4, 2005, 18:11:52
Job time : 670 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 4, 2005, 17:27:06 ; Search time 1551 Seconds
(without alignments)
4987.568 Million cell updates/sec

Title: US-10-066-521-6
Perfect score: 7074
Sequence: 1 MEGDKSLTFSSYGLQWCLYE.....DDHSGVSWSLGAAGLEGLVS 1344

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10066521/runat_04022005_114554_4440/app_query.fasta_1.1543
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=std.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10066521_@CGN_1_1_876_@runat_04022005_114554_4440
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7074	100.0	4035	14	US-10-124-498-5	Sequence 5, Appli
2	7074	100.0	4035	14	US-10-066-521-5	Sequence 5, Appli
3	5756	81.4	3489	17	US-10-416-642-3	Sequence 3, Appli
4	5756	81.4	3926	15	US-10-216-645-1	Sequence 1, Appli
5	5741.5	81.2	3885	18	US-10-860-761-3	Sequence 3, Appli
6	5741.5	81.2	3900	17	US-10-399-443-23	Sequence 23, Appl
7	5741.5	81.2	3900	17	US-10-677-943-23	Sequence 23, Appl
8	5683.5	80.3	3830	15	US-10-216-645-3	Sequence 3, Appli
9	5120	72.4	3226	17	US-10-092-900A-347	Sequence 347, App
10	2688	38.0	3447	17	US-10-399-443-5	Sequence 5, Appli
11	2688	38.0	3447	17	US-10-677-943-5	Sequence 5, Appli
12	2005	28.3	1157	17	US-10-399-443-1	Sequence 1, Appli
13	2005	28.3	1157	17	US-10-677-943-1	Sequence 1, Appli
14	1885.5	26.7	3521	18	US-10-794-342-2	Sequence 2, Appli
15	1435	20.3	3368	14	US-10-124-498-23	Sequence 23, Appl
16	1435	20.3	3368	14	US-10-066-521-23	Sequence 23, Appl
17	1434	20.3	2982	14	US-10-124-498-25	Sequence 25, Appl
18	1434	20.3	2982	14	US-10-066-521-25	Sequence 25, Appl
19	1434	20.3	2985	10	US-09-965-621-15	Sequence 15, Appl
20	1434	20.3	2985	17	US-10-407-866-15	Sequence 15, Appl
21	1434	20.3	2985	18	US-10-781-294-15	Sequence 15, Appl
22	1402	19.8	2775	17	US-10-357-820-51	Sequence 51, Appl
23	1335	18.9	1075	17	US-10-399-443-3	Sequence 3, Appli
24	1335	18.9	1075	17	US-10-677-943-3	Sequence 3, Appli
25	1332.5	18.8	3484	18	US-10-794-342-3	Sequence 3, Appli
26	1320.5	18.7	3108	10	US-09-965-621-23	Sequence 23, Appl
27	1320.5	18.7	3108	17	US-10-407-866-23	Sequence 23, Appl
28	1320.5	18.7	3108	18	US-10-781-294-23	Sequence 23, Appl
29	1316.5	18.6	3190	17	US-10-094-749-1079	Sequence 1079, Ap
30	1315.5	18.6	3172	18	US-10-398-037-74	Sequence 74, Appl
31	1314.5	18.6	2883	17	US-10-161-493-3	Sequence 3, Appli
32	1313.5	18.6	3540	18	US-10-794-342-7	Sequence 7, Appli
33	1304.5	18.4	3218	17	US-10-407-866-67	Sequence 67, Appl
34	1303.5	18.4	3186	14	US-10-124-498-17	Sequence 17, Appl
35	1303.5	18.4	3186	14	US-10-066-521-17	Sequence 17, Appl
36	1289.5	18.2	2575	9	US-09-848-035-7	Sequence 7, Appli
37	1289.5	18.2	2575	9	US-09-986-224-7	Sequence 7, Appli
38	1255	17.7	3102	13	US-10-127-516-6	Sequence 6, Appli
39	1255	17.7	3102	13	US-10-027-629-6	Sequence 6, Appli
40	1255	17.7	3102	16	US-10-132-967-6	Sequence 6, Appli
41	1255	17.7	3857	13	US-10-127-516-4	Sequence 4, Appli
42	1255	17.7	3857	13	US-10-027-629-4	Sequence 4, Appli
43	1255	17.7	3857	16	US-10-132-967-4	Sequence 4, Appli
44	1248.5	17.6	3189	15	US-10-239-663-10	Sequence 10, Appl
45	1242	17.6	3466	17	US-10-108-260A-718	Sequence 718, App

ALIGNMENTS

RESULT 1
US-10-124-498-5
; Sequence 5, Application US/10124498
; Publication No. US20030017983A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-367001
; CURRENT APPLICATION NUMBER: US/10/124,498
; CURRENT FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 10/066,521
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 4035
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(4032)
US-10-124-498-5

Alignment Scores:
Pred. No.:              0           Length:         4035
Score:                  7074.00     Matches:        1344
Percent Similarity:     100.00%     Conservative:   0
Best Local Similarity:  100.00%     Mismatches:     0
Query Match:            100.00%     Indels:         0
DB:                     14          Gaps:           0

US-10-066-521-6 (1-1344) x US-10-124-498-5 (1-4035)

Qy          1 MetGluGlyAspLysSerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysLysSerSerGluSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy         41 ThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy         61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy         81 AsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspAspMetLysLysIleSerGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300

Qy        101 AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGluIleSerGlnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360

Qy        121 MetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGlyHisGlyGlyAspThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420

Qy        141 TrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspValArgArgSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480

Qy        161 PheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540

Qy        181 AspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGlyIleGlyLys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600

Qy        201 SerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGlyLeuTyrGlnGlyMet 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660

Qy        221 PheSerTyrValPhePheLeuProValArgGluMetGlnArgLysLysGluSerSerVal 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720

Qy        241 ThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMetSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780

Qy        261 ArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsn 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840

Qy        281 AsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProProPheThrLeuIleArg 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900

Qy        301 SerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrValArgAspVal 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960

Qy        321 GlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuValArgGlyIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020

Qy        341 SerGlyGluGlnArgIleHisLeuLeuGluArgGlyIleGlyGluHisGlnLysThr 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080

Qy        361 GlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAla 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140

Qy        381 ValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyGluSerValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200

Qy        401 ProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrPro 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260

Qy        421 ArgGlyValValArgArgCysLeuAsnLeuGluGluArgValValLeuLysArgPheCys 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320

Qy        441 ArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyAspAspLeuMet 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380

Qy        461 ValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuPro 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440

Qy        481 AspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAla 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500

Qy        501 AlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeuCysProLeuTyrVal 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560

Qy        521 GluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620

Qy        541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680

Qy        561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeu 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740

Qy        581 GlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeuPhe 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800

Qy        601 GluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrpLeu 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860

Qy        621 ProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyr 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920
Qy        641 LeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerAlaGluAla 660
Db       1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980
Qy        661 CysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrpGluAsp 680
Db       1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040
Qy        681 PheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIle 700
Db       2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100
Qy        701 LeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCysLysIle 720
Db       2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160
Qy        721 GlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrpArgIle 740
Db       2161 CAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATC 2220
Qy        741 ValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGluGlu 760
Db       2221 GTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAG 2280
Qy        761 AspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSerLeuArg 780
Db       2281 GATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGG 2340
Qy        781 LeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThrThr 800
Db       2341 CTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACC 2400
Qy        801 SerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMet 820
Db       2401 TCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATG 2460
Qy        821 ProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAsp 840
Db       2461 CCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGAC 2520
Qy        841 CysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSer 860
Db       2521 TGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGC 2580
Qy        861 LeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeuCys 880
Db       2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640
Qy        881 ArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeu 900
Db       2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700
Qy        901 AspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHis 920
Db       2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760
Qy        921 LeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGluValMet 940
Db       2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820
Qy        941 ArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThrAlaAla 960
Db       2821 AGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCG 2880
Qy        961 CysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAspLeu 980
Db       2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940
Qy        981 ThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGlnLys 1000
Db       2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000

Qy       1001 AsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCysGlu 1020
Db       3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060
Qy       1021 AlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGlnAsn 1040
Db       3061 GCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAAT 3120
Qy       1041 AsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSerAsn 1060
Db       3121 AACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAAC 3180
Qy       1061 LeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleArgLysLeuGluGlu 1080
Db       3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240
Qy       1081 GluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHisSerPheAspGlu 1100
Db       3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300
Qy       1101 AspAspArgHisLysIleGlyLeuThrPheArgLeuProGluSerArgAlaTrpProCys 1120
Db       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360
Qy       1121 AlaLeuLeuTrpGlyMetAsnProGluGlnLysLysArgValSerLeuLeuAlaGlyAsp 1140
Db       3361 GCCTTGCTGTGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420
Qy       1141 PheLysSerSerThrArgPheAlaLysSerLeuCysLeuAlaThrAlaAsnGlyGluSer 1160
Db       3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480
Qy       1161 GlnArgValAspAsnValGluGlnSerSerProGlnProMetAlaGlyThrGluHisLys 1180
Db       3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540
Qy       1181 GlnAspLysMetLeuSerValGlyTyrSerGlyAlaTrpSerGluThrAlaGluLeuGlu 1200
Db       3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600
Qy       1201 GlyLeuGlySerAsnSerAlaAspHisAspHisGlyGlyMetAlaTrpSerLeuGlyArg 1220
Db       3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660
Qy       1221 GluLeuSerSerArgGlyLeuCysProThrValLeuMetThrThrAlaValCysProGly 1240
Db       3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720
Qy       1241 HisTrpGluArgLeuGlySerArgGlyTrpCysLeuAsnSerAlaAspAspHisSerGly 1260
Db       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780
Qy       1261 ValSerTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuValSerAsnSerAlaAspAsp 1280
Db       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840
Qy       1281 HisSerGlyValAlaTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuValSerAsnSer 1300
Db       3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900
Qy       1301 AlaAspAspHisSerGlyValSerTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuVal 1320
Db       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960
Qy       1321 SerAsnSerAlaAspAspHisSerGlyValSerTrpSerLeuGlyAlaAlaGlyLeuGlu 1340
Db       3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020
Qy       1341 GlyLeuValSer 1344
Db       4021 GGGCTGGTGTCT 4032
```

```
RESULT 2
US-10-066-521-5
; Sequence 5, Application US/10066521
; Publication No. US20030027757A1
; GENERAL INFORMATION:
;  APPLICANT: Bertin, John
;  APPLICANT:  Wang, Weiye
;  APPLICANT:  Blatcher, Maria
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
;  TITLE OF INVENTION:  PROTEIN FAMILY AND USES THEREOF
;  FILE REFERENCE: 07334-334001
;  CURRENT APPLICATION NUMBER: US/10/066,521
;  CURRENT FILING DATE:  2002-06-25
;  PRIOR APPLICATION NUMBER: 60/318,645
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: 60/265,231
;  PRIOR FILING DATE: 2001-01-31
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 4035
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(4032)
US-10-066-521-5

Alignment Scores:
Pred. No.:              0           Length:         4035
Score:                  7074.00     Matches:        1344
Percent Similarity:     100.00%     Conservative:   0
Best Local Similarity:  100.00%     Mismatches:     0
Query Match:            100.00%     Indels:         0
DB:                     14          Gaps:           0

US-10-066-521-6 (1-1344) x US-10-066-521-5 (1-4035)

Qy          1 MetGluGlyAspLysSerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysLysSerSerGluSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy         41 ThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy         61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy         81 AsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspAspMetLysLysIleSerGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300

Qy        101 AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGluIleSerGlnAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360

Qy        121 MetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGlyHisGlyGlyAspThr 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420

Qy        141 TrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspValArgArgSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480

Qy        161 PheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSer 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540

Qy        181 AspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGlyIleGlyLys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600

Qy        201 SerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGlyLeuTyrGlnGlyMet 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660

Qy        221 PheSerTyrValPhePheLeuProValArgGluMetGlnArgLysLysGluSerSerVal 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720

Qy        241 ThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMetSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780

Qy        261 ArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsn 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840

Qy        281 AsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProProPheThrLeuIleArg 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900

Qy        301 SerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrValArgAspVal 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960

Qy        321 GlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuValArgGlyIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020

Qy        341 SerGlyGluGlnArgIleHisLeuLeuLeuGluArgGlyIleGlyGluHisGlnLysThr 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080

Qy        361 GlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAla 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140

Qy        381 ValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyGluSerValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200

Qy        401 ProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrPro 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260

Qy        421 ArgGlyValValArgArgCysLeuAsnLeuGluGluArgValValLeuLysArgPheCys 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320

Qy        441 ArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyAspAspLeuMet 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380

Qy        461 ValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuPro 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440

Qy        481 AspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAla 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500

Qy        501 AlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeuCysProLeuTyrVal 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560

Qy        521 GluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620
```

```
Qy       541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560
Db      1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680

Qy       561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeu 580
Db      1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740

Qy       581 GlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeuPhe 600
Db      1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800

Qy       601 GluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrpLeu 620
Db      1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860

Qy       621 ProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyr 640
Db      1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920

Qy       641 LeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerAlaGluAla 660
Db      1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980

Qy       661 CysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrpGluAsp 680
Db      1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040

Qy       681 PheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIle 700
Db      2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100

Qy       701 LeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCysLysIle 720
Db      2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160

Qy       721 GlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrpArgIle 740
Db      2161 CAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATC 2220

Qy       741 ValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGluGlu 760
Db      2221 GTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAG 2280

Qy       761 AspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSerLeuArg 780
Db      2281 GATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGG 2340

Qy       781 LeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThrThr 800
Db      2341 CTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACC 2400

Qy       801 SerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMet 820
Db      2401 TCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATG 2460

Qy       821 ProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAsp 840
Db      2461 CCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGAC 2520

Qy       841 CysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSer 860
Db      2521 TGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGC 2580

Qy       861 LeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeuCys 880
Db      2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640

Qy       881 ArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeu 900
Db      2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700

Qy       901 AspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHis 920
```

```
Db      2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760

Qy       921 LeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGluValMet 940
Db      2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820

Qy       941 ArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThrAlaAla 960
Db      2821 AGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCG 2880

Qy       961 CysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAspLeu 980
Db      2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940

Qy       981 ThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGlnLys 1000
Db      2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000

Qy      1001 AsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCysGlu 1020
Db      3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060

Qy      1021 AlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGlnAsn 1040
Db      3061 GCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAAT 3120

Qy      1041 AsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSerAsn 1060
Db      3121 AACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAAC 3180

Qy      1061 LeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleArgLysLeuGluGlu 1080
Db      3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240

Qy      1081 GluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHisSerPheAspGlu 1100
Db      3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300

Qy      1101 AspAspArgHisLysIleGlyLeuThrPheArgLeuProGluSerArgAlaTrpProCys 1120
Db      3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360

Qy      1121 AlaLeuLeuTrpGlyMetAsnProGluGlnLysLysArgValSerLeuLeuAlaGlyAsp 1140
Db      3361 GCCTTGCTGTGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420

Qy      1141 PheLysSerSerThrArgPheAlaLysSerLeuCysLeuAlaThrAlaAsnGlyGluSer 1160
Db      3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480

Qy      1161 GlnArgValAspAsnValGluGlnSerSerProGlnProMetAlaGlyThrGluHisLys 1180
Db      3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540

Qy      1181 GlnAspLysMetLeuSerValGlyTyrSerGlyAlaTrpSerGluThrAlaGluLeuGlu 1200
Db      3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600

Qy      1201 GlyLeuGlySerAsnSerAlaAspHisAspHisGlyGlyMetAlaTrpSerLeuGlyArg 1220
Db      3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660

Qy      1221 GluLeuSerSerArgGlyLeuCysProThrValLeuMetThrThrAlaValCysProGly 1240
Db      3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720

Qy      1241 HisTrpGluArgLeuGlySerArgGlyTrpCysLeuAsnSerAlaAspAspHisSerGly 1260
Db      3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780

Qy      1261 ValSerTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuValSerAsnSerAlaAspAsp 1280
```

```
Db       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840

Qy       1281 HisSerGlyValAlaTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuValSerAsnSer 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900

Qy       1301 AlaAspAspHisSerGlyValSerTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuVal 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960

Qy       1321 SerAsnSerAlaAspAspHisSerGlyValSerTrpSerLeuGlyAlaAlaGlyLeuGlu 1340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020

Qy       1341 GlyLeuValSer 1344
              ||||||||||||
Db       4021 GGGCTGGTGTCT 4032

RESULT 3
US-10-416-642-3
; Sequence 3, Application US/10416642
; Publication No. US20040043452A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  ARVIZU, Chandra
;  TITLE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS
;  FILE REFERENCE: PF-0842 PCT
;  CURRENT APPLICATION NUMBER: US/10/416,642
;  CURRENT FILING DATE:  2003-05-13
;  PRIOR APPLICATION NUMBER: 60/249,407
;  PRIOR FILING DATE: 2000-11-15
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PERL Program
; SEQ ID NO 3
;   LENGTH: 3489
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040043452A1 7474830CB1
US-10-416-642-3

Alignment Scores:
Pred. No.:              0              Length:         3489
Score:                  5756.00        Matches:        1102
Percent Similarity:     95.34%         Conservative:   2
Best Local Similarity:  95.16%         Mismatches:     0
Query Match:            81.37%         Indels:         54
DB:                     17             Gaps:           1

US-10-066-521-6 (1-1344) x US-10-416-642-3 (1-3489)

Qy          1 MetGluGlyAspLysSerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysLysSerSerGluSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy         41 ThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy         61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy         81 AsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspAspMetLys------------ 96
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAATTCACCAGAA 300

Qy         96 ------------------------------------------------------------ 96

Db        301 GATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGAAAATAAA 360

Qy         96 ------------------------------------------------------------ 96

Db        361 TATGGCATGACTAAGCTTATCTTGGGGGTGTCTGACATCTCTGACTCGAATAATAAACAC 420

Qy         97 ----------------------------LysIleSerGlnAlaMetGluGlnGluGly 106
                                           :::||||||||||||||||||||||||||||
Db        421 AAGTATGTTGGAATTCATTCTTCTTTTGCAGAAATTTCACAAGCTATGGAACAAGAAGGT 480

Qy        107 AlaThrAlaAlaGluThrGluGluGlnGluIleSerGlnAlaMetGluGlnGluGlyAla 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCC 540

Qy        127 ThrAlaAlaGluThrGluGluGlnGlyHisGlyGlyAspThrTrpAspTyrLysSerHis 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGTCAC 600

Qy        147 ValMetThrLysPheAlaGluGluGluAspValArgArgSerPheGluAsnThrAlaAla 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCT 660

Qy        167 AspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSerAspArgTrpGlyPheArg 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGG 720

Qy        187 ProArgThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArg 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGG 780

Qy        207 IleValLeuCysTrpAlaGlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePhe 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTC 840

Qy        227 LeuProValArgGluMetGlnArgLysLysGluSerSerValThrGluPheIleSerArg 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGG 900

Qy        247 GluTrpProAspSerGlnAlaProValThrGluIleMetSerArgProGluArgLeuLeu 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTG 960

Qy        267 PheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAsnAspThrLysLeuCys 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGC 1020

Qy        287 LysAspTrpAlaGluLysGlnProProPheThrLeuIleArgSerLeuLeuArgLysVal 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTC 1080

Qy        307 LeuLeuProGluSerPheLeuIleValThrValArgAspValGlyThrGluLysLeuLys 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAG 1140

Qy        327 SerGluValValSerProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIle 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATC 1200

Qy        347 HisLeuLeuLeuGluArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIle 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATC 1260

Qy        367 MetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCys 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGC 1320

Qy        387 ValAlaLeuGlnLeuGlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeu 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCCTTCAACCAAACGCTC 1380

Qy        407 ThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValArgArg 426
```

```
Db       1381 ACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGC 1440
Qy        427 CysLeuAsnLeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGly 446
Db       1441 TGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGA 1500
Qy        447 ValTrpAsnArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGlu 466
Db       1501 GTGTGGAATAGGAAGTCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAG 1560
Qy        467 SerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCysGluGlu 486
Db       1561 TCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAG 1620
Qy        487 TyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeu 506
Db       1621 TACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTA 1680
Qy        507 GluGlyLeuGluIleGluProAlaLeuCysProLeuTyrValGluLysThrLysArgSer 526
Db       1681 GAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCC 1740
Qy        527 MetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrpMetLysArgPheLeuPhe 546
Db       1741 ATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTT 1800
Qy        547 GlyLeuValSerGluAspValArgArgProLeuGluValLeuLeuGlyCysProValPro 566
Db       1801 GGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCC 1860
Qy        567 LeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeuGlyGlnGlnProAsnAla 586
Db       1861 CTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCC 1920
Qy        587 ThrThrProGlyAspThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGlu 606
Db       1921 ACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAG 1980
Qy        607 PheValArgLeuAlaLeuAsnSerPheGlnGluValTrpLeuProIleAsnGlnAsnLeu 626
Db       1981 TTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTG 2040
Qy        627 AspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArgVal 646
Db       2041 GACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTG 2100
Qy        647 AspValLysGlyIlePheProArgAspGluSerAlaGluAlaCysProValValProLeu 666
Db       2101 GATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTA 2160
Qy        667 TrpMetArgAspLysThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGly 686
Db       2161 TGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGC 2220
Qy        687 ThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMet 706
Db       2221 ACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATG 2280
Qy        707 LysThrLeuCysAlaLysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArg 726
Db       2281 AAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGA 2340
Qy        727 AsnAlaGlnIleThrProGlyValGlnHisLeuTrpArgIleValMetAlaAsnArgAsn 746
Db       2341 AATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAAC 2400
Qy        747 LeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGluGluAspValArgMetAlaCys 766
Db       2401 CTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGT 2460
Qy        767 GluAlaLeuLysHisProLysCysLeuLeuGluSerLeuArgLeuAspCysCysGlyLeu 786
Db       2461 GAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTG 2520
Qy        787 ThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSer 806
Db       2521 ACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCT 2580
Qy        807 LeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeu 826
Db       2581 CTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTG 2640
Qy        827 ArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAlaThr 846
Db       2641 AGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACG 2700
Qy        847 GlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeu 866
Db       2701 GGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTA 2760
Qy        867 SerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeuPro 886
Db       2761 TCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCC 2820
Qy        887 HisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGly 906
Db       2821 CACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGT 2880
Qy        907 PheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsn 926
Db       2881 TTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAAC 2940
Qy        927 ProValGluAspAsnGlyValLysLeuLeuCysGluValMetArgGluProSerCysHis 946
Db       2941 CCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCAT 3000
Qy        947 LeuGlnAspLeuGluLeuValLysCysHisLeuThrAlaAlaCysCysGluSerLeuSer 966
Db       3001 CTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCC 3060
Qy        967 CysValIleSerArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGly 986
Db       3061 TGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGT 3120
Qy        987 AspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGlnLysAsnSerValLeuThrArg 1006
Db       3121 GACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGA 3180
Qy       1007 LeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeu 1026
Db       3181 CTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTT 3240
Qy       1027 SerCysAsnArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGly 1046
Db       3241 TCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGA 3300
Qy       1047 MetMetLysLeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeu 1066
Db       3301 ATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTG 3360
Qy       1067 TrpLysTrpGlnTyrProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuLys 1086
Db       3361 TGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAG 3420
Qy       1087 ProArgValValIleAspGlySerTrpHisSerPheAspGluAspAspArgHis 1104
Db       3421 CCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGGTAC 3474

RESULT 4
US-10-216-645-1
; Sequence 1, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
;  APPLICANT: WEISS, BERTRAM
;  APPLICANT:  LESSL, MONIKA
```

```
;  APPLICANT:  PETERS-KOTTIG, MICHAELE
;  APPLICANT:  BECKMANN, GEORG
;  TITLE OF INVENTION: HUMAN MATER PROTEINS
;  FILE REFERENCE: SCH-1910
;  CURRENT APPLICATION NUMBER: US/10/216,645
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 3926
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-216-645-1

Alignment Scores:
Pred. No.:              0           Length:         3926
Score:                  5756.00     Matches:        1102
Percent Similarity:     95.34%      Conservative:   2
Best Local Similarity:  95.16%      Mismatches:     0
Query Match:            81.37%      Indels:         54
DB:                     15          Gaps:           1

US-10-066-521-6 (1-1344) x US-10-216-645-1 (1-3926)

Qy          1 MetGluGlyAspLysSerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysLysSerSerGluSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy         41 ThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy         61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy         81 AsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspAspMetLys------------ 96
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAATTCACCAGAA 300

Qy         96 ------------------------------------------------------------ 96

Db        301 GATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGAAAATAAA 360

Qy         96 ------------------------------------------------------------ 96

Db        361 TATGGCATGACTAAGCTTATCTTGGGGGTGTCTGACATCTCTGACTCGAATAATAAACAC 420

Qy         97 ------------------------------LysIleSerGlnAlaMetGluGlnGluGly 106
                                           :::||||||||||||||||||||||||||||
Db        421 AAGTATGTTGGAATTCATTCTTCTTTTGCAGAAATTTCACAAGCTATGGAACAAGAAGGT 480

Qy        107 AlaThrAlaAlaGluThrGluGluGlnGluIleSerGlnAlaMetGluGlnGluGlyAla 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCC 540

Qy        127 ThrAlaAlaGluThrGluGluGlnGlyHisGlyGlyAspThrTrpAspTyrLysSerHis 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGTCAC 600

Qy        147 ValMetThrLysPheAlaGluGluGluAspValArgArgSerPheGluAsnThrAlaAla 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCT 660

Qy        167 AspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSerAspArgTrpGlyPheArg 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGG 720

Qy        187 ProArgThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArg 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGG 780

Qy        207 IleValLeuCysTrpAlaGlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePhe 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTC 840

Qy        227 LeuProValArgGluMetGlnArgLysLysGluSerSerValThrGluPheIleSerArg 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGG 900

Qy        247 GluTrpProAspSerGlnAlaProValThrGluIleMetSerArgProGluArgLeuLeu 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTG 960

Qy        267 PheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAsnAspThrLysLeuCys 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGC 1020

Qy        287 LysAspTrpAlaGluLysGlnProProPheThrLeuIleArgSerLeuLeuArgLysVal 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTC 1080

Qy        307 LeuLeuProGluSerPheLeuIleValThrValArgAspValGlyThrGluLysLeuLys 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAG 1140

Qy        327 SerGluValValSerProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIle 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATC 1200

Qy        347 HisLeuLeuLeuGluArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIle 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATC 1260

Qy        367 MetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCys 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGC 1320

Qy        387 ValAlaLeuGlnLeuGlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeu 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTC 1380

Qy        407 ThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValArgArg 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGC 1440

Qy        427 CysLeuAsnLeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGly 446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGA 1500

Qy        447 ValTrpAsnArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGlu 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GTGTGGAATAGGAAGTCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAG 1560

Qy        467 SerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCysGluGlu 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAG 1620

Qy        487 TyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeu 506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTA 1680

Qy        507 GluGlyLeuGluIleGluProAlaLeuCysProLeuTyrValGluLysThrLysArgSer 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCC 1740

Qy        527 MetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrpMetLysArgPheLeuPhe 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 ATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTT 1800
```

```
Qy       547 GlyLeuValSerGluAspValArgArgProLeuGluValLeuLeuGlyCysProValPro 566
Db      1801 GGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCC 1860

Qy       567 LeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeuGlyGlnGlnProAsnAla 586
Db      1861 CTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCC 1920

Qy       587 ThrThrProGlyAspThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGlu 606
Db      1921 ACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAG 1980

Qy       607 PheValArgLeuAlaLeuAsnSerPheGlnGluValTrpLeuProIleAsnGlnAsnLeu 626
Db      1981 TTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTG 2040

Qy       627 AspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArgVal 646
Db      2041 GACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTG 2100

Qy       647 AspValLysGlyIlePheProArgAspGluSerAlaGluAlaCysProValValProLeu 666
Db      2101 GATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTA 2160

Qy       667 TrpMetArgAspLysThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGly 686
Db      2161 TGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGC 2220

Qy       687 ThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMet 706
Db      2221 ACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATG 2280

Qy       707 LysThrLeuCysAlaLysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArg 726
Db      2281 AAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGA 2340

Qy       727 AsnAlaGlnIleThrProGlyValGlnHisLeuTrpArgIleValMetAlaAsnArgAsn 746
Db      2341 AATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAAC 2400

Qy       747 LeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGluGluAspValArgMetAlaCys 766
Db      2401 CTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGT 2460

Qy       767 GluAlaLeuLysHisProLysCysLeuLeuGluSerLeuArgLeuAspCysCysGlyLeu 786
Db      2461 GAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTG 2520

Qy       787 ThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSer 806
Db      2521 ACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCT 2580

Qy       807 LeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeu 826
Db      2581 CTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTG 2640

Qy       827 ArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAlaThr 846
Db      2641 AGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACG 2700

Qy       847 GlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeu 866
Db      2701 GGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTA 2760

Qy       867 SerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeuPro 886
Db      2761 TCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCC 2820

Qy       887 HisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGly 906
Db      2821 CACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGT 2880

Qy       907 PheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsn 926
Db      2881 TTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAAC 2940

Qy       927 ProValGluAspAsnGlyValLysLeuLeuCysGluValMetArgGluProSerCysHis 946
Db      2941 CCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCAT 3000

Qy       947 LeuGlnAspLeuGluLeuValLysCysHisLeuThrAlaAlaCysCysGluSerLeuSer 966
Db      3001 CTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCC 3060

Qy       967 CysValIleSerArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGly 986
Db      3061 TGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGT 3120

Qy       987 AspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGlnLysAsnSerValLeuThrArg 1006
Db      3121 GACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGA 3180

Qy      1007 LeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeu 1026
Db      3181 CTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTT 3240

Qy      1027 SerCysAsnArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGly 1046
Db      3241 TCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGA 3300

Qy      1047 MetMetLysLeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeu 1066
Db      3301 ATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTG 3360

Qy      1067 TrpLysTrpGlnTyrProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuLys 1086
Db      3361 TGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAG 3420

Qy      1087 ProArgValValIleAspGlySerTrpHisSerPheAspGluAspAspArgHis 1104
Db      3421 CCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGGTAC 3474
```

RESULT 5
US-10-860-761-3
; Sequence 3, Application US/10860761
; Publication No. US20040248775A1
; GENERAL INFORMATION:
; APPLICANT: WYETH
; TITLE OF INVENTION: METHODS FOR SCREENING INHIBITORS OF APOPTOSIS
; FILE REFERENCE: AM101318
; CURRENT APPLICATION NUMBER: US/10/860,761
; CURRENT FILING DATE: 2004-06-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 3885
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3603)
US-10-860-761-3

Alignment Scores:

Pred. No.:	0	Length:	3885
Score:	5741.50	Matches:	1098
Percent Similarity:	96.16%	Conservative:	3
Best Local Similarity:	95.90%	Mismatches:	3
Query Match:	81.16%	Indels:	41
DB:	18	Gaps:	1

US-10-066-521-6 (1-1344) x US-10-860-761-3 (1-3885)

```
Qy         1 MetGluGlyAspLysSerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGlu 20
Db       154 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 213
```

```
Qy        21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysLysSerSerGluSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       214 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 273

Qy        41 ThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       274 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 333

Qy        61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       334 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 393

Qy        81 AsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspAspMetLysLys--------- 97
             ||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       394 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAGACATTCACCA 453

Qy        97 ------------------------------------------------------------ 97

Db       454 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 513

Qy        98 ------------------------------------------------------IleSer 99
                                                                     ||||||
Db       514 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGAGACAAAAGAACAGGAAATTTCA 573

Qy       100 GlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGluIleSerGln 119
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       574 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 633

Qy       120 AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGlyHisGlyGlyAsp 139
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       634 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 693

Qy       140 ThrTrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspValArgArg 159
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       694 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 753

Qy       160 SerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAsp 179
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       754 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 813

Qy       180 SerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGlyIleGly 199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       814 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 873

Qy       200 LysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGlyLeuTyrGlnGly 219
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       874 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 933

Qy       220 MetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLysLysGluSerSer 239
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       934 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 993

Qy       240 ValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMet 259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       994 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 1053

Qy       260 SerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeu 279
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1054 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 1113

Qy       280 AsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProProPheThrLeuIle 299
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 1173

Qy       300 ArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrValArgAsp 319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 1233

Qy       320 ValGlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuValArgGly 339
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1234 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1293

Qy       340 IleSerGlyGluGlnArgIleHisLeuLeuLeuGluArgGlyIleGlyGluHisGlnLys 359
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1294 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1353

Qy       360 ThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValPro 379
             ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db      1354 ACACAAGGGTTGCGTGCGATCATCAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1413

Qy       380 AlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyGluSerVal 399
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1414 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1473

Qy       400 AlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThr 419
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1474 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGCGTTTCATCAGCTCACC 1533

Qy       420 ProArgGlyValValArgArgCysLeuAsnLeuGluGluArgValValLeuLysArgPhe 439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1534 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1593

Qy       440 CysArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyAspAspLeu 459
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1594 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1653

Qy       460 MetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeu 479
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1654 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1713

Qy       480 ProAspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCys 499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1714 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1773

Qy       500 AlaAlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeuCysProLeuTyr 519
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1774 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1833

Qy       520 ValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeu 539
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1834 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1893

Qy       540 TrpMetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluVal 559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1894 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1953

Qy       560 LeuLeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeu 579
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1954 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 2013

Qy       580 LeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeu 599
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2014 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 2073

Qy       600 PheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrp 619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2074 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 2133

Qy       620 LeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysPro 639
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2134 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 2193

Qy       640 TyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerAlaGlu 659
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2194 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 2253

Qy       660 AlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrpGlu 679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2254 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2313

Qy       680 AspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSer 699
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2314 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2373

Qy       700 IleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCysLys 719
```

```
Db       2374 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2433

Qy        720 IleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrpArg 739

Db       2434 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACCTCTGGAGA 2493

Qy        740 IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGlu 759

Db       2494 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2553

Qy        760 GluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSerLeu 779

Db       2554 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2613

Qy        780 ArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThr 799

Db       2614 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2673

Qy        800 ThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyVal 819

Db       2674 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2733

Qy        820 MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGlu 839

Db       2734 ACGCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2793

Qy        840 AspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859

Db       2794 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2853

Qy        860 SerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeu 879

Db       2854 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2913

Qy        880 CysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899

Db       2914 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2973

Qy        900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThr 919

Db       2974 CTGGACACGGCTGGCTGTGGTTCTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 3033

Qy        920 HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGluVal 939

Db       3034 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 3093

Qy        940 MetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThrAla 959

Db       3094 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 3153

Qy        960 AlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAsp 979

Db       3154 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 3213

Qy        980 LeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGln 999

Db       3214 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 3273

Qy       1000 LysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCys 1019

Db       3274 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3333

Qy       1020 GluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGln 1039

Db       3334 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3393

Qy       1040 AsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSer 1059

Db       3394 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3453

Qy       1060 AsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleArgLysLeuLeu 1079

Db       3454 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3513

Qy       1080 GluGluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHisSerPheAsp 1099

Db       3514 GAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGAT 3573

Qy       1100 GluAspAspArgHis 1104

Db       3574 GAAGATGACCGGTAC 3588
```

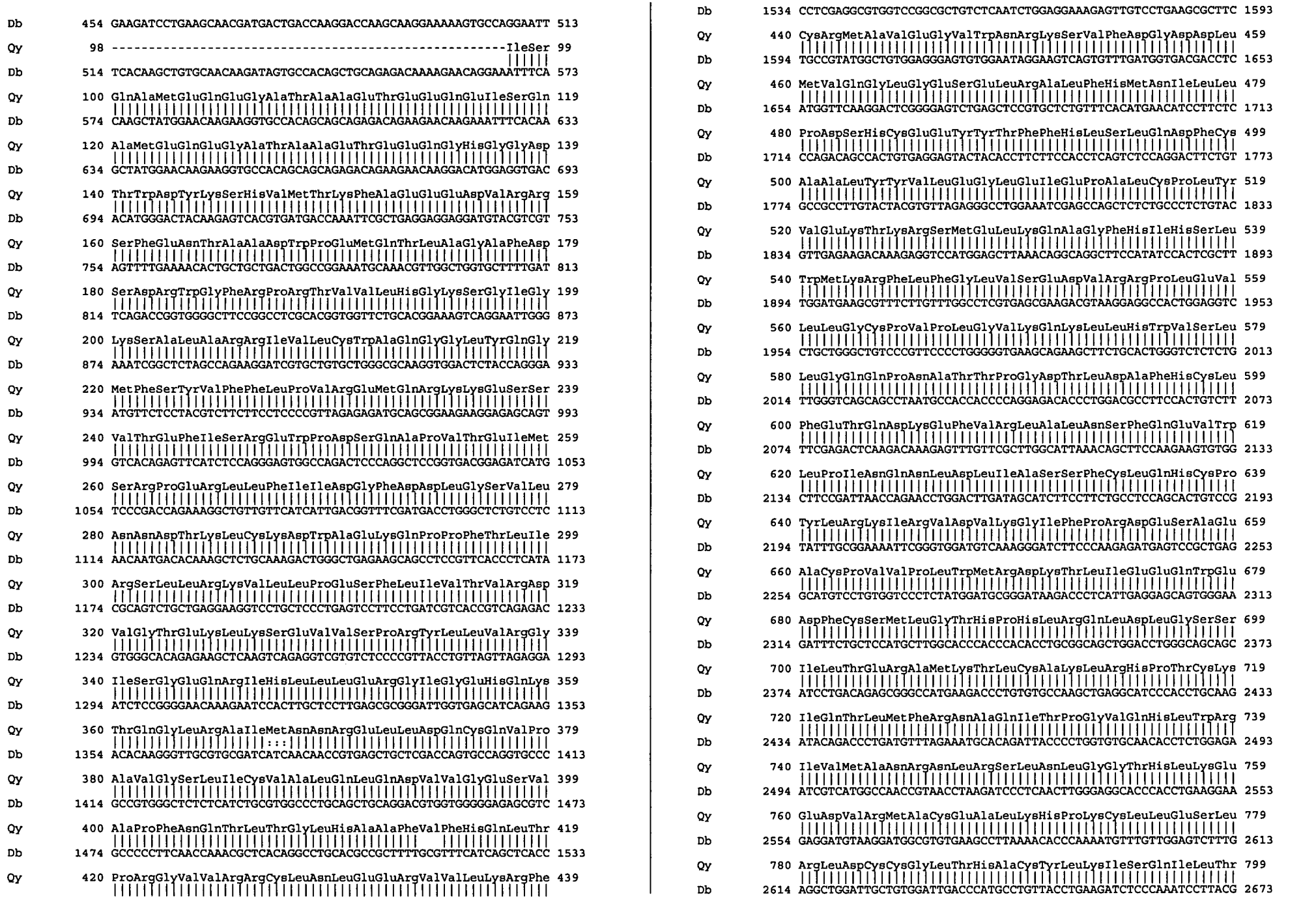
RESULT 6
US-10-399-443-23
; Sequence 23, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3600)
; OTHER INFORMATION:
US-10-399-443-23

Alignment Scores:

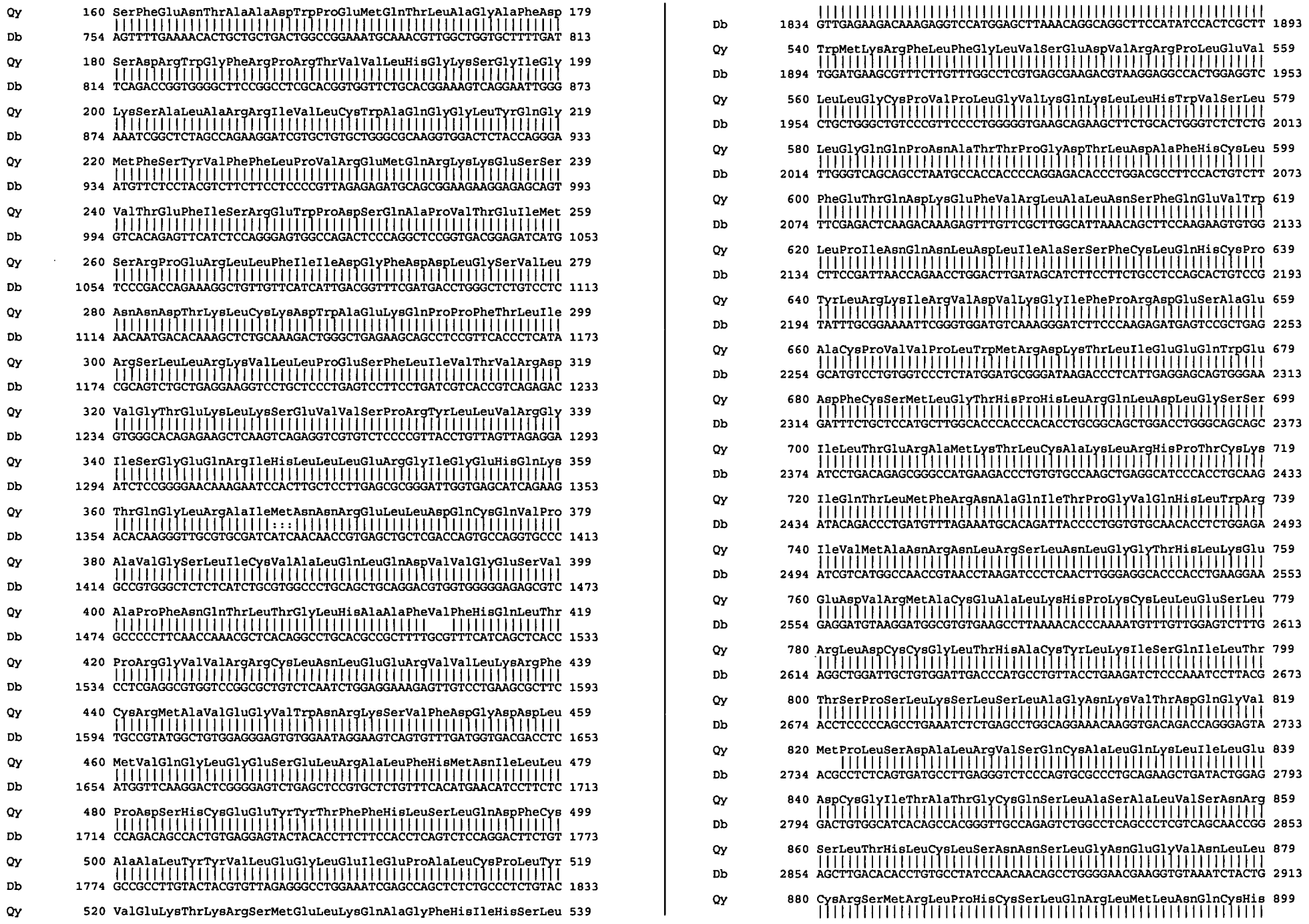
Pred. No.:	0	Length:	3900
Score:	5741.50	Matches:	1098
Percent Similarity:	96.16%	Conservative:	3
Best Local Similarity:	95.90%	Mismatches:	3
Query Match:	81.16%	Indels:	41
DB:	17	Gaps:	1

US-10-066-521-6 (1-1344) x US-10-399-443-23 (1-3900)

```
Qy          1 MetGluGlyAspLysSerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGlu 20

Db        154 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 213

Qy         21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysLysSerSerGluSer 40

Db        214 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 273

Qy         41 ThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeu 60

Db        274 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 333

Qy         61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80

Db        334 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 393

Qy         81 AsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspAspMetLysLys--------- 97

Db        394 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAGACATTCACCA 453

Qy         97 ------------------------------------------------------------ 97
```


Db 454 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 513
Qy 98 ----------IleSer 99
Db 514 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGAGACAAAAGAACAGGAAATTTCA 573
Qy 100 GlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGluIleSerGln 119
Db 574 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 633
Qy 120 AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGlyHisGlyGlyAsp 139
Db 634 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 693
Qy 140 ThrTrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspValArgArg 159
Db 694 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 753
Qy 160 SerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAsp 179
Db 754 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 813
Qy 180 SerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGlyIleGly 199
Db 814 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 873
Qy 200 LysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGlyLeuTyrGlnGly 219
Db 874 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 933
Qy 220 MetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLysLysGluSerSer 239
Db 934 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 993
Qy 240 ValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMet 259
Db 994 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 1053
Qy 260 SerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeu 279
Db 1054 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 1113
Qy 280 AsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProProPheThrLeuIle 299
Db 1114 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 1173
Qy 300 ArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrValArgAsp 319
Db 1174 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 1233
Qy 320 ValGlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuValArgGly 339
Db 1234 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1293
Qy 340 IleSerGlyGluGlnArgIleHisLeuLeuLeuGluArgGlyIleGlyGluHisGlnLys 359
Db 1294 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1353
Qy 360 ThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValPro 379
Db 1354 ACACAAGGGTTGCGTGCGATCATCAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1413
Qy 380 AlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyGluSerVal 399
Db 1414 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1473
Qy 400 AlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThr 419
Db 1474 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGCGTTTCATCAGCTCACC 1533
Qy 420 ProArgGlyValValArgArgCysLeuAsnLeuGluGluArgValValLeuLysArgPhe 439
Db 1534 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1593
Qy 440 CysArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyAspAspLeu 459
Db 1594 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1653
Qy 460 MetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeu 479
Db 1654 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1713
Qy 480 ProAspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCys 499
Db 1714 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1773
Qy 500 AlaAlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeuCysProLeuTyr 519
Db 1774 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1833
Qy 520 ValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeu 539
Db 1834 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1893
Qy 540 TrpMetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluVal 559
Db 1894 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1953
Qy 560 LeuLeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeu 579
Db 1954 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 2013
Qy 580 LeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeu 599
Db 2014 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 2073
Qy 600 PheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrp 619
Db 2074 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 2133
Qy 620 LeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysPro 639
Db 2134 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 2193
Qy 640 TyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerAlaGlu 659
Db 2194 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 2253
Qy 660 AlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrpGlu 679
Db 2254 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2313
Qy 680 AspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSer 699
Db 2314 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2373
Qy 700 IleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCysLys 719
Db 2374 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2433
Qy 720 IleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrpArg 739
Db 2434 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACCTCTGGAGA 2493
Qy 740 IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGlu 759
Db 2494 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2553
Qy 760 GluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSerLeu 779
Db 2554 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2613
Qy 780 ArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThr 799
Db 2614 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2673

```
Qy        800 ThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyVal 819
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2733

Qy        820 MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGlu 839
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2734 ACGCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2793

Qy        840 AspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2794 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2853

Qy        860 SerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeu 879
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2854 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2913

Qy        880 CysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2914 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2973

Qy        900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThr 919
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db       2974 CTGGACACGGCTGGCTGTGGTTCTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 3033

Qy        920 HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGluVal 939
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3034 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 3093

Qy        940 MetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThrAla 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3094 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 3153

Qy        960 AlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAsp 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 3213

Qy        980 LeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGln 999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3214 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 3273

Qy       1000 LysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCys 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3274 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3333

Qy       1020 GluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGln 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3334 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3393

Qy       1040 AsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSer 1059
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3394 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3453

Qy       1060 AsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleArgLysLeuLeu 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3454 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3513

Qy       1080 GluGluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHisSerPheAsp 1099
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3514 GAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGAT 3573

Qy       1100 GluAspAspArgHis 1104
              ||||||||||||:::
Db       3574 GAAGATGACCGGTAC 3588

RESULT 7
US-10-677-943-23
; Sequence 23, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
;   LENGTH: 3900
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3600)
US-10-677-943-23

Alignment Scores:
Pred. No.:                0              Length:          3900
Score:                    5741.50        Matches:         1098
Percent Similarity:       96.16%         Conservative:    3
Best Local Similarity:    95.90%         Mismatches:      3
Query Match:              81.16%         Indels:          41
DB:                       17             Gaps:            1

US-10-066-521-6 (1-1344) x US-10-677-943-23 (1-3900)

Qy          1 MetGluGlyAspLysSerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 213

Qy         21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysLysSerSerGluSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 273

Qy         41 ThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 333

Qy         61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 393

Qy         81 AsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspAspMetLysLys--------- 97
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        394 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAGACATTCACCA 453

Qy         97 ------------------------------------------------------------ 97

Db        454 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 513

Qy         98 ----------------------------------------------------------IleSer 99
                                                                         ||||||
Db        514 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGAGACAAAAGAACAGGAAATTTCA 573

Qy        100 GlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGluIleSerGln 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 633

Qy        120 AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGlyHisGlyGlyAsp 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 693

Qy        140 ThrTrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspValArgArg 159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 753
```


Qy 160 SerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAsp 179
Db 754 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 813
Qy 180 SerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGlyIleGly 199
Db 814 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 873
Qy 200 LysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGlyLeuTyrGlnGly 219
Db 874 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 933
Qy 220 MetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLysLysGluSerSer 239
Db 934 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 993
Qy 240 ValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMet 259
Db 994 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 1053
Qy 260 SerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeu 279
Db 1054 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 1113
Qy 280 AsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProProPheThrLeuIle 299
Db 1114 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 1173
Qy 300 ArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrValArgAsp 319
Db 1174 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 1233
Qy 320 ValGlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuValArgGly 339
Db 1234 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1293
Qy 340 IleSerGlyGluGlnArgIleHisLeuLeuLeuGluArgGlyIleGlyGluHisGlnLys 359
Db 1294 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1353
Qy 360 ThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValPro 379
Db 1354 ACACAAGGGTTGCGTGCGATCATCAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1413
Qy 380 AlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyGluSerVal 399
Db 1414 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1473
Qy 400 AlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThr 419
Db 1474 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGCGTTTCATCAGCTCACC 1533
Qy 420 ProArgGlyValValArgArgCysLeuAsnLeuGluGluArgValValLeuLysArgPhe 439
Db 1534 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1593
Qy 440 CysArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyAspAspLeu 459
Db 1594 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1653
Qy 460 MetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeu 479
Db 1654 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1713
Qy 480 ProAspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCys 499
Db 1714 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1773
Qy 500 AlaAlaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeuCysProLeuTyr 519
Db 1774 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1833
Qy 520 ValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeu 539
Db 1834 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1893
Qy 540 TrpMetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluVal 559
Db 1894 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1953
Qy 560 LeuLeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeu 579
Db 1954 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 2013
Qy 580 LeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeu 599
Db 2014 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 2073
Qy 600 PheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrp 619
Db 2074 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 2133
Qy 620 LeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysPro 639
Db 2134 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 2193
Qy 640 TyrLeuArgLysIleArgValAspValLysGlyIleProArgAspGluSerAlaGlu 659
Db 2194 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 2253
Qy 660 AlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrpGlu 679
Db 2254 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2313
Qy 680 AspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSer 699
Db 2314 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2373
Qy 700 IleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCysLys 719
Db 2374 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2433
Qy 720 IleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrpArg 739
Db 2434 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACCTCTGGAGA 2493
Qy 740 IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGlu 759
Db 2494 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2553
Qy 760 GluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSerLeu 779
Db 2554 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2613
Qy 780 ArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThr 799
Db 2614 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2673
Qy 800 ThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyVal 819
Db 2674 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2733
Qy 820 MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGlu 839
Db 2734 ACGCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2793
Qy 840 AspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
Db 2794 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2853
Qy 860 SerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeu 879
Db 2854 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2913
Qy 880 CysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899

```
Db       2914 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2973

Qy        900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThr 919
              |||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db       2974 CTGGACACGGCTGGCTGTGGTTCTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 3033

Qy        920 HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGluVal 939
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3034 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 3093

Qy        940 MetArgGluProSerCysHisLeuGlnAspLeuGluLeuValLysCysHisLeuThrAla 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3094 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 3153

Qy        960 AlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAsp 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 3213

Qy        980 LeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGln 999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3214 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 3273

Qy       1000 LysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCys 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3274 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3333

Qy       1020 GluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGln 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3334 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3393

Qy       1040 AsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSer 1059
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3394 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3453

Qy       1060 AsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProValGlnIleArgLysLeuLeu 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3454 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3513

Qy       1080 GluGluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHisSerPheAsp 1099
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3514 GAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGAT 3573

Qy       1100 GluAspAspArgHis 1104
              |||||||||||:::
Db       3574 GAAGATGACCGGTAC 3588

RESULT 8
US-10-216-645-3
; Sequence 3, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
;  APPLICANT: WEISS, BERTRAM
;  APPLICANT:  LESSL, MONIKA
;  APPLICANT:  PETERS-KOTTIG, MICHAELE
;  APPLICANT:  BECKMANN, GEORG
;  TITLE OF INVENTION: HUMAN MATER PROTEINS
;  FILE REFERENCE: SCH-1910
;  CURRENT APPLICATION NUMBER: US/10/216,645
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 3830
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-216-645-3

Alignment Scores:
Pred. No.:              0           Length:         3830
Score:                  5683.50     Matches:        1087
Percent Similarity:     95.87%      Conservative:   5
Best Local Similarity:  95.43%      Mismatches:     12
Query Match:            80.34%      Indels:         35
DB:                     15          Gaps:           2

US-10-066-521-6 (1-1344) x US-10-216-645-3 (1-3830)

Qy          1 MetGluGlyAspLysSerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysLysSerSerGluSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy         41 ThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy         61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy         81 AsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspAspMetLysLysIleSerGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAATTCACCAGAA 300

Qy        101 ------------AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGln--- 115
                          |||   :::|||  :::     :::     |||
Db        301 GATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGAAAATAAA 360

Qy        115 ------------------------------------------------------------ 115

Db        361 TATGGCATGACTAAGCTTATCTTGGGGGTGTCTGACATCTCTGACTCGAATAATAAACAC 420

Qy        116 ----------------------------GluIleSerGlnAlaMetGluGlnGluGly 125
                                         ||||||||||||||||||||||||||||||
Db        421 AAGTATGTTGGAATTCATTCTTCTTTTGCAGAAATTTCACAAGCTATGGAACAAGAAGGT 480

Qy        126 AlaThrAlaAlaGluThrGluGluGlnGlyHisGlyGlyAspThrTrpAspTyrLysSer 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGT 540

Qy        146 HisValMetThrLysPheAlaGluGluGluAspValArgArgSerPheGluAsnThrAla 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCT 600

Qy        166 AlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSerAspArgTrpGlyPhe 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTC 660

Qy        186 ArgProArgThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArg 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGA 720

Qy        206 ArgIleValLeuCysTrpAlaGlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhe 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTC 780

Qy        226 PheLeuProValArgGluMetGlnArgLysLysGluSerSerValThrGluPheIleSer 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCC 840

Qy        246 ArgGluTrpProAspSerGlnAlaProValThrGluIleMetSerArgProGluArgLeu 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTG 900

Qy        266 LeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAsnAspThrLysLeu 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTC 960

Qy        286 CysLysAspTrpAlaGluLysGlnProProPheThrLeuIleArgSerLeuLeuArgLys 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAG 1020
```

```
Qy       306 ValLeuLeuProGluSerPheLeuIleValThrValArgAspValGlyThrGluLysLeu 325
Db      1021 GTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTC 1080

Qy       326 LysSerGluValValSerProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArg 345
Db      1081 AAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGA 1140

Qy       346 IleHisLeuLeuLeuGluArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAla 365
Db      1141 ATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCG 1200

Qy       366 IleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIle 385
Db      1201 ATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATC 1260

Qy       386 CysValAlaLeuGlnLeuGlnAspValValGlyGluSerValAlaProPheAsnGlnThr 405
Db      1261 TGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACG 1320

Qy       406 LeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValArg 425
Db      1321 CTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGG 1380

Qy       426 ArgCysLeuAsnLeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGlu 445
Db      1381 CGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAG 1440

Qy       446 GlyValTrpAsnArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGly 465
Db      1441 GGAGTGTGGAATAGGAAGTCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGG 1500

Qy       466 GluSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCysGlu 485
Db      1501 GAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAG 1560

Qy       486 GluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrVal 505
Db      1561 GAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTG 1620

Qy       506 LeuGluGlyLeuGluIleGluProAlaLeuCysProLeuTyrValGluLysThrLysArg 525
Db      1621 TTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGG 1680

Qy       526 SerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrpMetLysArgPheLeu 545
Db      1681 TCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTG 1740

Qy       546 PheGlyLeuValSerGluAspValArgArgProLeuGluValLeuLeuGlyCysProVal 565
Db      1741 TTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTT 1800

Qy       566 ProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeuGlyGlnGlnProAsn 585
Db      1801 CCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAAT 1860

Qy       586 AlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLys 605
Db      1861 GCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAA 1920

Qy       606 GluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrpLeuProIleAsnGlnAsn 625
Db      1921 GAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAAC 1980

Qy       626 LeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArg 645
Db      1981 CTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGG 2040

Qy       646 ValAspValLysGlyIlePheProArgAspGluSerAlaGluAlaCysProValValPro 665
Db      2041 GTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCT 2100

Qy       666 LeuTrpMetArgAspLysThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeu 685
Db      2101 CTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTT 2160

Qy       686 GlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAla 705
Db      2161 GGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCC 2220

Qy       706 MetLysThrLeuCysAlaLysLeuArgHisProThrCysLysIleGlnThrLeuMetPhe 725
Db      2221 ATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTT 2280

Qy       726 ArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrpArgIleValMetAlaAsnArg 745
Db      2281 AGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGT 2340

Qy       746 AsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGluGluAspValArgMetAla 765
Db      2341 AACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCG 2400

Qy       766 CysGluAlaLeuLysHisProLysCysLeuGluSerLeuArgLeuAspCysCysGly 785
Db      2401 TGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGA 2460

Qy       786 LeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLys 805
Db      2461 TTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAA 2520

Qy       806 SerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAla 825
Db      2521 TCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCC 2580

Qy       826 LeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAla 845
Db      2581 TTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCC 2640

Qy       846 ThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCys 865
Db      2641 ACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGC 2700

Qy       866 LeuSerAsnAsnSerLeuGlyAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeu 885
Db      2701 CTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTT 2760

Qy       886 ProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCys 905
Db      2761 CCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGT 2820

Qy       906 GlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMet 925
Db      2821 GGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATG 2880

Qy       926 AsnProValGluAspAsnGlyValLysLeuLeuCysGluValMetArgGluProSerCys 945
Db      2881 AACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGT 2940

Qy       946 HisLeuGlnAspLeuGluLeuValLysCysHisLeuThrAlaAlaCysCysGluSerLeu 965
Db      2941 CATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTG 3000

Qy       966 SerCysValIleSerArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeu 985
Db      3001 TCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTG 3060

Qy       986 GlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGlnLysAsnSerValLeuThr 1005
Db      3061 GGTGACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACG 3120

Qy      1006 ArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAla 1025
Db      3121 AGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCC 3180

Qy      1026 LeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLys 1045
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAA 3240

Qy       1046 GlyMetMetLysLeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGly 1065
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 GGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGG 3300

Qy       1066 LeuTrpLysTrpGlnTyrProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeu 1085
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 CTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTC 3360

Qy       1086 LysProArgValValIleAspGlySerTrpHisSerPheAspGluAspAspArgHis 1104
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       3361 AAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGGTAC 3417

RESULT 9
US-10-092-900A-347
; Sequence 347, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
;  APPLICANT: Padigaru, Muralidhara
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Taupier Jr., Raymond J.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Li, Li
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Ji, Weizhen
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Guo, Xiaojia Sasha
;  APPLICANT:  Tchernev,, Velizar T.
;  APPLICANT:  Fernandes, Elma R.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Liu, Yi
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Catterton, Elina
;  APPLICANT:  Leite, Mario W.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Alsobrook, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: No. US20040043382Alel Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-290C
;  CURRENT APPLICATION NUMBER: US/10/092,900A
;  CURRENT FILING DATE:  2002-03-07
;  PRIOR APPLICATION NUMBER: USSN 60/274,322
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/283,675
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: USSN 60/338,092
;  PRIOR FILING DATE: 2001-12-03
;  PRIOR APPLICATION NUMBER: USSN 60/274,281
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/274,191
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/325,681
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: USSN 60/304,354
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: USSN 60/279,995
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: USSN 60/294,899
;  PRIOR FILING DATE: 2001-05-31
;  PRIOR APPLICATION NUMBER: USSN 60/287,424
;  PRIOR FILING DATE: 2001-04-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 347
;   LENGTH: 3226
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (69)..(3168)
US-10-092-900A-347

Alignment Scores:
Pred. No.:                0              Length:          3226
Score:                    5120.00        Matches:         977
Percent Similarity:       96.95%         Conservative:    7
Best Local Similarity:    96.26%         Mismatches:      20
Query Match:              72.38%         Indels:          11
DB:                       17             Gaps:            1

US-10-066-521-6 (1-1344) x US-10-092-900A-347 (1-3226)

Qy        101 AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGluIleSerGlnAla 120
                |||     ::::::          ||||||||||||     :::      :::
Db        113 GCCCAAAGGGAGAAGGCTCAGGCCACGGCAGAGACGGAACCAGGAAAACGTCACGAAAAA 172

Qy        121 MetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGln-Gly---------- 135
                  |||          :::   |||   |||:::       |||
Db        173 CAGCCTCAAGTTGCCAGGTCCCTTGCAGGAACAGACAGGCCTGGGGCCGCCCCACCTGGG 232

Qy        136 ----------------HisGlyGlyAspThrTrpAspTyrLysSerHisValMetThrLy 150
                             ||||||||||||||||||||||||||||||||||||||||||
Db        233 CTCAGAGCTTGGGCTGCATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAA 292

Qy        150 sPheAlaGluGluGluAspValArgArgSerPheGluAsnThrAlaAlaAspTrpProGl 170
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 ATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGA 352

Qy        170 uMetGlnThrLeuAlaGlyAlaPheAspSerAspArgTrpGlyPheArgProArgThrVa 190
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 AATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGT 412

Qy        190 lValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCy 210
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTG 472

Qy        210 sTrpAlaGlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValAr 230
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 CTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAG 532

Qy        230 gGluMetGlnArgLysLysGluSerSerValThrGluPheIleSerArgGluTrpProAs 250
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGA 592

Qy        250 pSerGlnAlaProValThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAs 270
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 CTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGA 652

Qy        270 pGlyPheAspAspLeuGlySerValLeuAsnAsnAspThrLysLeuCysLysAspTrpAl 290
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 CGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGC 712

Qy        290 aGluLysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGl 310
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 TGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGA 772

Qy        310 uSerPheLeuIleValThrValArgAspValGlyThrGluLysLeuLysSerGluValVa 330
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 GTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGT 832

Qy        330 lSerProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLe 350
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        833 GTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCT 892

Qy        350 uGluArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnAr 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 TGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCG 952

Qy        370 gGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGl 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        953 TGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCA 1012

Qy        390 nLeuGlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeuThrGlyLeuHi 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1013 GCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCA 1072

Qy        410 sAlaAlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLe 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1073 CGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCT 1132

Qy        430 uGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsnAr 450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1133 GGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAG 1192

Qy        450 gLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuAr 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1193 GAAGTCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCG 1252

Qy        470 gAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCysGluGluTyrTyrThrPh 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1253 TGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTT 1312

Qy        490 ePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGl 510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1313 CTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGA 1372

Qy        510 uIleGluProAlaLeuCysProLeuTyrValGluLysThrLysArgSerMetGluLeuLy 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1373 AATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAA 1432

Qy        530 sGlnAlaGlyPheHisIleHisSerLeuTrpMetLysArgPheLeuPheGlyLeuValSe 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1433 ACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAG 1492

Qy        550 rGluAspValArgArgProLeuGluValLeuLeuGlyCysProValProLeuGlyValLy 570
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1493 CGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAA 1552

Qy        570 sGlnLysLeuLeuHisTrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGl 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1553 GCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGG 1612

Qy        590 yAspThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLe 610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1613 AGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTT 1672

Qy        610 uAlaLeuAsnSerPheGlnGluValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAl 630
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1673 GGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGC 1732

Qy        630 aSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArgValAspValLysGl 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1733 ATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGG 1792

Qy        650 yIlePheProArgAspGluSerAlaGluAlaCysProValValProLeuTrpMetArgAs 670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1793 GATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGA 1852

Qy        670 pLysThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGlyThrHisProHi 690
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1853 TAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACA 1912

Qy        690 sLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLysThrLeuCy 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1913 CCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTG 1972

Qy        710 sAlaLysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIl 730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1973 TGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGAT 2032

Qy        730 eThrProGlyValGlnHisLeuTrpArgIleValMetAlaAsnArgAsnLeuArgSerLe 750
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2033 TACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCT 2092

Qy        750 uAsnLeuGlyGlyThrHisLeuLysGluGluAspValArgMetAlaCysGluAlaLeuLy 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2093 CAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAA 2152

Qy        770 sHisProLysCysLeuLeuGluSerLeuArgLeuAspCysCysGlyLeuThrHisAlaCy 790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2153 ACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTG 2212

Qy        790 sTyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeuAl 810
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2213 TTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGC 2272

Qy        810 aGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGl 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2273 AGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCA 2332

Qy        830 nCysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAlaThrGlyCysGlnSe 850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2333 GTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAG 2392

Qy        850 rLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSe 870
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2393 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 2452

Qy        870 rLeuGlyAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLe 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2453 CCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCT 2512

Qy        890 uGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLe 910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2513 GCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACT 2572

Qy        910 uAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAs 930
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2573 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 2632

Qy        930 pAsnGlyValLysLeuLeuCysGluValMetArgGluProSerCysHisLeuGlnAspLe 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2633 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 2692

Qy        950 uGluLeuValLysCysHisLeuThrAlaAlaCysCysGluSerLeuSerCysValIleSe 970
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2693 GGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 2752

Qy        970 rArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyVa 990
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2753 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 2812

Qy        990 lAlaAlaLeuCysGluGlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLy 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2813 TGCTGCACTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 2872

Qy       1010 sAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnAr 1030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2873 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 2932

Qy       1030 gHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLe 1050
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2933 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 2992

Qy       1050 uCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGl 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2993 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 3052
```

```
Qy       1070 nTyrProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuLysProArgValVa 1090
Db       3053 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 3112

Qy       1090 lIleAspGlySerTrpHisSerPheAspGluAspAspArgHis 1104
Db       3113 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGGTAC 3155

RESULT 10
US-10-399-443-5
; Sequence 5, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as Represented by the
;  APPLICANT:  Secretary, Department of Health & Human Services, The National Institute
;  APPLICANT:  Health
;  APPLICANT:  Nelson, Lawrence M.
;  APPLICANT:  Tong, Zhi-Bin
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Zhi-Bin, Tong
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64785
;  CURRENT APPLICATION NUMBER: US/10/399,443
;  CURRENT FILING DATE:  2003-04-16
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 3447
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-399-443-5

Alignment Scores:
Pred. No.:              8.76e-276       Length:         3447
Score:                  2688.00         Matches:        554
Percent Similarity:     66.49%          Conservative:   186
Best Local Similarity:  49.78%          Mismatches:     293
Query Match:            38.00%          Indels:         81
DB:                     17              Gaps:           11

US-10-066-521-6 (1-1344) x US-10-399-443-5 (1-3447)

Qy         15 GlnTrpCysLeuTyrGluLeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLys 34
Db        163 CAATGGGTCCTCCA-GAAAAAGACAGTAAAGCAATCTTGAAAGCACGTGGATTGGAAGAG 221

Qy         35 LysLysSerSerGluSerThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsn 54
Db        222 GAACAGAAGTCAGAAAGCACA---------------------------------------- 242

Qy         55 ValGluCysLeuAlaLeuLeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThr 74
Db        242 ---------------------------------------------------------- 242

Qy         75 SerIleSerIlePheGluAsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspAsp 94
Db        243 ---ATGTCTCCTTCAGAAAATGTCAGTAGAGCAATCCTGAAAGACAGTGGATCAGAAGAA 299

Qy         95 MetLysLysIleSerGln---------------------------------------- 100
Db        300 GTGGAACAGGCGTCAGAAAGAAAAATGACTTCTCCAGAAAACGACAGTAAATCAATCCAG 359

Qy        101 --------------AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGln 115
Db        360 AAAGACCAAGGACCAGAGCAGGAGCAGACATCAGAAACCTTACAATCTAAGGAAGAAGAT 419

Qy        116 GluIleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGly 135
Db        420 GAAGTGACAGAGGCA----------------------------------GATAAAGAT 443

Qy        136 HisGlyGlyAspThrTrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGlu 155
Db        444 AATGGAGGTGACTTACAAGACTACAAGGCCCATGTGATTGCTAAGTTCGACACAAGTGTG 503

Qy        156 AspValArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAla 175
Db        504 GATCTACAC--------------------TATGACAGCCCAGAGATGAAAATTATTGTCT 542

Qy        176 GlyAlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLys 195
Db        543 GATGCTTTTAAACCATACCAGAAAACCTTCCAGCCTCACACCATTATCCTACATGGAAGA 602

Qy        196 SerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGly 215
Db        603 CCAGGAGTTGGGAAGTCAGCTTTGGCCAGAAGTATTGTTCTTGGCTGGGCACAGGGTAAA 662

Qy        216 LeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLys 235
Db        663 CTCTTCCAAAAAATG---TCCTTTGTCATCTTCTTCTCTGTTAGAGAAATAAAGTGGACA 719

Qy        236 LysGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProVal 255
Db        720 GAGAAGAGCAGTTTGGCACAGCTGATTGCTAAGGAGTGTCCAGACTCCTGGGATCTAGTG 779

Qy        256 ThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeu 275
Db        780 ACAAAGATCATGTCCCAACCAGAAAGACTCTTGTTTGTCATAGATGGCTTGGATGATATG 839

Qy        276 GlySerValLeu---AsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnPro 294
Db        840 GACTCTGTCCTCCAACATGATGATATGACACTATCCAGAGACTGGAAGGATGAACAGCCC 899

Qy        295 ProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIle 314
Db        900 ATATACATCCTGATGTACAGCCTCCTGAGGAAGGCTCTCTTACCTCAGTCCTTTCTCATC 959

Qy        315 ValThrValArgAspValGlyThrGluLysLeuLysSerGluValValSerProArgTyr 334
Db        960 ATTACCACCAGAAACACAGGCTTAGAAAAACTCAAGTCAATGGTTGTGTCCCCCCTCTAT 1019

Qy        335 LeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGluArgGlyIle 354
Db       1020 ATACTGGTTGAAGGACTGTCTGCATCAAGGAGATCTCAGCTGGTCCTCGAGAACATCTCC 1079

Qy        355 GlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAsp 374
Db       1080 AATGAGTCTGATAGAATACAAGTCTTCCATTCTCTGATAGAAAATCACCAGCTGTTTGAC 1139

Qy        375 GlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspVal 394
Db       1140 CAATGCCAGGCCCCCTCTGTGTGCTCCCTGGTCTGTGAGGCTCTACAGCTACAGAAGAAA 1199

Qy        395 ValGlyGluSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheVal 414
Db       1200 CTGGGAAAGAGATGCACCCTACCCTGCCAGACTCTCACCGGTTTGTATGCCACGTTGGTG 1259

Qy        415 PheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGluGluArgVal 434
Db       1260 TTTCACCAGCTCACCTTGAAAAGGCCTTCCCAGAGCGCTCTCAGTCAGGAAGAACAGATT 1319

Qy        435 ValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerValPhe 454
Db       1320 ACTCTAGTGGGTTTGTGCATGATGGCAGCTGAAGGAGTGTGGACCATGAGGTCGGTGTTC 1379

Qy        455 AspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHis 474
Db       1380 TATGATGATGACCTGAAGAACTATAGCCTAAAGGAGTCTGAGATCTTGGCCCTCTTTCAC 1439

Qy        475 MetAsnIleLeuLeuProAspSerHis---CysGluGluTyrTyrThrPhePheHisLeu 493
Db       1440 ATGAACATCCTTCTCCAGGTTGGCCACAACAGTGAGCAGTGTTATGTTTTCTCCCACCTC 1499
```

```
Qy       494 SerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeu---GluIleGlu 512
Db      1500 AGCCTGCAGGATTTCTTTGCTGCCTTATATTATGTTTTAGAAGGGCTGGAGGAATGGAAT 1559

Qy       513 ProAlaLeuCysProLeuTyrValGluLysThrLysArgSerMetGluLeuLysGlnAla 532
Db      1560 CAGCATTTTTGC------TTCATTGAAAACCAAAGGAGCATCATGGAGGTGAAGAGAACT 1613

Qy       533 GlyPheHisIleHisSerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGluAsp 552
Db      1614 GAC---GACACTCGCCTCCTCGGGATGAAGCGTTTCTTATTTGGCCTCATGAACAAGGAT 1670

Qy       553 ValArgArgProLeuGluValLeuLeuGlyCysProValProLeuGlyValLysGlnLys 572
Db      1671 ATCTTGAAGACTCTGGAGGTTCTGTTTGAATATCCCGTGATTCCAACTGTTGAGCAGAAG 1730

Qy       573 LeuLeuHisTrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThr 592
Db      1731 CTCCAACACTGGGTCTCTCTGATAGCTCAGCAGGTCAATGGCACCAGCCCAATGGACACC 1790

Qy       593 LeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeu 612
Db      1791 CTGGATGCCTTCTATTGTCTATTTGAGTCTCAGGATGAAGAGTTTGTTGGCGGGGCTCTC 1850

Qy       613 AsnSerPheGlnGluValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSer 632
Db      1851 AAACGCTTCCAAGAAGTGTGGCTGCTGATTAACCAGAAGATGGACTTGAAGGTCTCTTCC 1910

Qy       633 PheCysLeuGlnHisCysProTyrLeuArgLysIleArgValAspValLysGlyIlePhe 652
Db      1911 TACTGTCTCAAGCACTGTCAGAACTTGAAGGCAATCCGGGTGGATATCAGAGACCTCCTC 1970

Qy       653 ProArgAspGluSerAlaGluAlaCysProValValProLeuTrp---MetArgAspLys 671
Db      1971 TCGGTAGATAATACTCTCGAGCTGTGCCCTGTTGTTACTGTCCAGGAGACACAATGTAAG 2030

Qy       672 ThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGlyThrHisProHisLeu 691
Db      2031 CCCCTCCTCATGGAGTGGTGGGGAAACTTCTGCTCTGTGCTTGGCAGCCTCCGGAACTTG 2090

Qy       692 ArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLysThrLeuCysAla 711
Db      2091 AAGGAGCTGGACTTGGGCGACAGCATCCTGAGTCAACGGGCCATGAAGATACTGTGCCTC 2150

Qy       712 LysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThr 731
Db      2151 GAGCTGCGGAATCAGTCCTGCAGAATACAGAAGCTGACGTTTAAGAGTGCAGAGGTAGTG 2210

Qy       732 ProGlyValGlnHisLeuTrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsn 751
Db      2211 TCTGGCCTGAAACATCTCTGGAAGCTCCTTTTTAGCAATCAAAACTTAAAGTACCTCAAT 2270

Qy       752 LeuGlyGlyThrHisLeuLysGluGluAspValArgMetAlaCysGluAlaLeuLysHis 771
Db      2271 CTAGGGAACACTCCCATGAAGGATGATGACATGAAGTTAGCCTGCGAAGCGCTGAAACAT 2330

Qy       772 ProLysCysLeuLeuGluSerLeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyr 791
Db      2331 CCAAAGTGCTCCGTGGAGACTCTGAGGTTGGATTCCTGTGAGTTAACCATCATTGGTTAT 2390

Qy       792 LeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGly 811
Db      2391 GAGATGATCTCCACGCTTCTTATTTCAACCACCAGGCTAAAGTGTCTCAGCCTGGCCAAA 2450

Qy       812 AsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGlnCys 831
Db      2451 AATAGAGTGGGAGTAAAAAGCATGATATCCCTTGGGAATGCCTTGAGTAGCTCAATGTGT 2510

Qy       832 AlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAlaThrGlyCysGlnSerLeu 851
Db      2511 CTACTGCAAAAGTTGATACTGGACAACTGTGGCCTCACACCTGCCAGCTGCCACCTTCTG 2570

Qy       852 AlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeu 871
Db      2571 GTCTCAGCCCTTTTCAGCAACCAGAACTTGACACACCTGTGCCTGTCAAACAACAGCCTG 2630

Qy       872 GlyAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeuGln 891
Db      2631 GGGACTGAAGGAGTGCAACAGCTGTGTCAGTTCCTGAGGAATCCAGAATGTGCTCTCCAG 2690

Qy       892 ArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAla 911
Db      2691 CGGCTGATACTGAATCACTGCAACATTGTAGATGATGCTTATGGCTTCCTGGCAATGAGA 2750

Qy       912 LeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAspAsn 931
Db      2751 CTTGCAAACAACACAAAGCTGACCCACCTGAGCCTGACCATGAACCCCGTAGGGGATGGT 2810

Qy       932 GlyValLysLeuLeuCysGluValMetArgGluProSerCysHisLeuGlnAspLeuGlu 951
Db      2811 GCAATGAAGCTACTGTGTGAAGCTTTAAAGGAACCTACTTGTTACCTTCAAGAACTGGAA 2870

Qy       952 LeuValLysCysHisLeuThrAlaAlaCysCysGluSerLeuSerCysValIleSerArg 971
Db      2871 CTAGTGGACTGCCAACTCACACAGAACTGCTGCGAGGACCTGGCCTGTATGATCACAACA 2930

Qy       972 SerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyValAla 991
Db      2931 ACCAAGCACTTAAAAAGTTTGGATCTTGGTAACAACGCCCTGGGTGACAAAGGAGTCATA 2990

Qy       992 AlaLeuCysGluGlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAla 1011
Db      2991 ACCCTGTGTGAGGGACTGAAGCAAAGTAGCAGCTCCCTGAGGAGACTTGGGTTGGGGGCA 3050

Qy      1012 CysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArgHis 1031
Db      3051 TGTAAGTTGACTTCCAATTGCTGTGAGGCATTGTCATTGGCCATCTCTTGCAACCCTCAC 3110

Qy      1032 LeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCys 1051
Db      3111 CTGAACAGCCTAAACCTGGTGAAGAATGACTTCAGTACATCGGGGATGTTGAAGCTGTGC 3170

Qy      1052 SerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyr 1071
Db      3171 TCTGCGTTCCAATGCCCTGTCTCTAACCTGGGGATAATTGGCCTGTGGAAGCAGGAGTAC 3230

Qy      1072 ProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuLysProArgValValIle 1091
Db      3231 TATGCCCGAGTGAGAAGACAGCTGGAGGAAGTTGAGTTTGTCAAGCCCCACGTGGTGATT 3290

Qy      1092 AspGlySerTrpHisSerPheAspGluAspAspArgHis 1104
Db      3291 GATGGTGATTGGTATGCTAGTGATGAAGATGACCGAAAC 3329
```

RESULT 11
US-10-677-943-5
; Sequence 5, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677,943
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2

```
; SEQ ID NO 5
;   LENGTH: 3447
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-677-943-5

Alignment Scores:
Pred. No.:              8.76e-276       Length:         3447
Score:                  2688.00         Matches:        554
Percent Similarity:     66.49%          Conservative:   186
Best Local Similarity:  49.78%          Mismatches:     293
Query Match:            38.00%          Indels:         81
DB:                     17              Gaps:           11

US-10-066-521-6 (1-1344) x US-10-677-943-5 (1-3447)

Qy          15 GlnTrpCysLeuTyrGluLeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLys 34
               ||||||  |||  |||  |||  :::                :::  |||  :::
Db         163 CAATGGGTCCTCCA-GAAAAAGACAGTAAAGCAATCTTGAAAGCACGTGGATTGGAAGAG 221

Qy          35 LysLysSerSerGluSerThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsn 54
               ::::::  ||||||||||||
Db         222 GAACAGAAGTCAGAAAGCACA---------------------------------------- 242

Qy          55 ValGluCysLeuAlaLeuLeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThr 74

Db         242 ------------------------------------------------------------ 242

Qy          75 SerIleSerIlePheGluAsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspAsp 94
                 :::|||      ||||||::::::        |||  :::       ::::::
Db         243 ---ATGTCTCCTTCAGAAAATGTCAGTAGAGCAATCCTGAAAGACAGTGGATCAGAAGAA 299

Qy          95 MetLysLysIleSerGln---------------------------------------- 100
               :::::::::  |||:::
Db         300 GTGGAACAGGCGTCAGAAAGAAAAATGACTTCTCCAGAAAACGACAGTAAATCAATCCAG 359

Qy         101 --------------AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGln 115
                           ||||||     |||          ||||||
Db         360 AAAGACCAAGGACCAGAGCAGGAGCAGACATCAGAAACCTTACAATCTAAGGAAGAAGAT 419

Qy         116 GluIleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGly 135
               |||::::::::::|||                                  ::::::
Db         420 GAAGTGACAGAGGCA----------------------------------GATAAAGAT 443

Qy         136 HisGlyGlyAspThrTrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGlu 155
               :::||||||||||     |||||||||:::||||||:::   ||||||
Db         444 AATGGAGGTGACTTACAAGACTACAAGGCCCATGTGATTGCTAAGTTCGACACAAGTGTG 503

Qy         156 AspValArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAla 175
               |||:::                        |||   ||||||||:::   |||:::
Db         504 GATCTACAC--------------------TATGACAGCCCAGAGATGAAATTATTGTCT 542

Qy         176 GlyAlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLys 195
                  ||||||        :::      |||:::|||   |||::::::|||||||:::
Db         543 GATGCTTTTAAACCATACCAGAAAACCTTCCAGCCTCACACCATTATCCTACATGGAAGA 602

Qy         196 SerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGly 215
                  |||:::||||||||||||||||||||||   |||||||||   ||||||||||||
Db         603 CCAGGAGTTGGGAAGTCAGCTTTGGCCAGAAGTATTGTTCTTGGCTGGGCACAGGGTAAA 662

Qy         216 LeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLys 235
               |||:::|||   |||   |||:::|||   |||       ||||||||||::::::
Db         663 CTCTTCCAAAAAATG---TCCTTTGTCATCTTCTTCTCTGTTAGAGAAATAAAGTGGACA 719

Qy         236 LysGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProVal 255
               ::::::||||||:::   :::   |||::::::|||   |||||||||          |||
Db         720 GAGAAGAGCAGTTTGGCACAGCTGATTGCTAAGGAGTGTCCAGACTCCTGGGATCTAGTG 779

Qy         256 ThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeu 275
               |||:::|||||||||:::|||||||||||||||||||:::|||||||||   ||||||:::
Db         780 ACAAAGATCATGTCCCAACCAGAAAGACTCTTGTTTGTCATAGATGGCTTGGATGATATG 839

Qy         276 GlySerValLeu---AsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnPro 294
```

```
                  |||||||||  ::::::|||      |||   :::||||||   ::::::||||||
Db         840 GACTCTGTCCTCCAACATGATGATATGACACTATCCAGAGACTGGAAGGATGAACAGCCC 899

Qy         295 ProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIle 314
                  :::   |||:::   ||||||||||||||   ||||||||||:::||||||||||||
Db         900 ATATACATCCTGATGTACAGCCTCCTGAGGAAGGCTCTCTTACCTCAGTCCTTTCTCATC 959

Qy         315 ValThrValArgAspValGlyThrGluLysLeuLysSerGluValValSerProArgTyr 334
               :::|||   |||:::   |||   ||||||||||||||   ||||||||||||   |||
Db         960 ATTACCACCAGAAACACAGGCTTAGAAAAACTCAAGTCAATGGTTGTGTCCCCCCTCTAT 1019

Qy         335 LeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGluArgGlyIle 354
               :::||||||   |||:::|||      :::|||      |||:::||||||
Db        1020 ATACTGGTTGAAGGACTGTCTGCATCAAGGAGATCTCAGCTGGTCCTCGAGAACATCTCC 1079

Qy         355 GlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAsp 374
                  |||      :::   |||         :::::::::   |||   :::|||   |||
Db        1080 AATGAGTCTGATAGAATACAAGTCTTCCATTCTCTGATAGAAAATCACCAGCTGTTTGAC 1139

Qy         375 GlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspVal 394
               |||||||||   |||:::|||   |||||||:::|||   ||||||||||||||||
Db        1140 CAATGCCAGGCCCCCTCTGTGTGCTCCCTGGTCTGTGAGGCTCTACAGCTACAGAAGAAA 1199

Qy         395 ValGlyGluSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheVal 414
               :::|||:::                |||||||||||||||||:::|||      |||
Db        1200 CTGGGAAAGAGATGCACCCTACCCTGCCAGACTCTCACCGGTTTGTATGCCACGTTGGTG 1259

Qy         415 PheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGluGluArgVal 434
               ||||||||||||||   :::         :::      |||:::   ||||||::::::
Db        1260 TTTCACCAGCTCACCTTGAAAAGGCCTTCCCAGAGCGCTCTCAGTCAGGAAGAACAGATT 1319

Qy         435 ValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerValPhe 454
                  |||      |||   ||||||   ||||||||||||      :::||||||||||
Db        1320 ACTCTAGTGGGTTTGTGCATGATGGCAGCTGAAGGAGTGTGGACCATGAGGTCGGTGTTC 1379

Qy         455 AspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHis 474
                     |||||||||         |||   |||||||||:::   ||||||||||||
Db        1380 TATGATGATGACCTGAAGAACTATAGCCTAAAGGAGTCTGAGATCTTGGCCCTCTTTCAC 1439

Qy         475 MetAsnIleLeuLeuProAspSerHis---CysGluGluTyrTyrThrPhePheHisLeu 493
               ||||||||||||||||         |||   |||:::   |||   |||   ||||||
Db        1440 ATGAACATCCTTCTCCAGGTTGGCCACAACAGTGAGCAGTGTTATGTTTTCTCCCACCTC 1499

Qy         494 SerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeu---GluIleGlu 512
               ||||||||||||||   ||||||||||||||||||||||||||||||   |||
Db        1500 AGCCTGCAGGATTTCTTTGCTGCCTTATATTATGTTTTAGAAGGGCTGGAGGAATGGAAT 1559

Qy         513 ProAlaLeuCysProLeuTyrValGluLysThrLysArgSerMetGluLeuLysGlnAla 532
                     |||      :::::::|||      :::      ||||||:::|||:::
Db        1560 CAGCATTTTTGC------TTCATTGAAAACCAAAGGAGCATCATGGAGGTGAAGAGAACT 1613

Qy         533 GlyPheHisIleHisSerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGluAsp 552
                        |||   ||||||||||||||||||||||||||:::::::::|||
Db        1614 GAC---GACACTCGCCTCCTCGGGATGAAGCGTTTCTTATTTGGCCTCATGAACAAGGAT 1670

Qy         553 ValArgArgProLeuGluValLeuLeuGlyCysProValProLeuGlyValLysGlnLys 572
               :::  :::   ||||||||||||      ||||||      |||:::||||||
Db        1671 ATCTTGAAGACTCTGGAGGTTCTGTTTGAATATCCCGTGATTCCAACTGTTGAGCAGAAG 1730

Qy         573 LeuLeuHisTrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThr 592
               |||   ||||||||||||||:::   ||||||   |||   |||:::|||   ||||||
Db        1731 CTCCAACACTGGGTCTCTCTGATAGCTCAGCAGGTCAATGGCACCAGCCCAATGGACACC 1790

Qy         593 LeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeu 612
               |||||||||||||:::|||||||||:::||||||:::|||||||||          ||||||
Db        1791 CTGGATGCCTTCTATTGTCTATTTGAGTCTCAGGATGAAGAGTTTGTTGGCGGGGCTCTC 1850

Qy         613 AsnSerPheGlnGluValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSer 632
                     ||||||||||||||||   |||||||||   :::||||||      ||||||
Db        1851 AAACGCTTCCAAGAAGTGTGGCTGCTGATTAACCAGAAGATGGACTTGAAGGTCTCTTCC 1910

Qy         633 PheCysLeuGlnHisCysProTyrLeuArgLysIleArgValAspValLysGlyIlePhe 652
               :::||||||:::||||||      |||:::   ||||||||||||::::::   :::
```

```
Db       1911 TACTGTCTCAAGCACTGTCAGAACTTGAAGGCAATCCGGGTGGATATCAGAGACCTCCTC 1970

Qy        653 ProArgAspGluSerAlaGluAlaCysProValValProLeuTrp---MetArgAspLys 671

Db       1971 TCGGTAGATAATACTCTCGAGCTGTGCCCTGTTGTTACTGTCCAGGAGACACAATGTAAG 2030

Qy        672 ThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGlyThrHisProHisLeu 691

Db       2031 CCCCTCCTCATGGAGTGGTGGGGAAACTTCTGCTCTGTGCTTGGCAGCCTCCGGAACTTG 2090

Qy        692 ArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLysThrLeuCysAla 711

Db       2091 AAGGAGCTGGACTTGGGCGACAGCATCCTGAGTCAACGGGCCATGAAGATACTGTGCCTC 2150

Qy        712 LysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThr 731

Db       2151 GAGCTGCGGAATCAGTCCTGCAGAATACAGAAGCTGACGTTTAAGAGTGCAGAGGTAGTG 2210

Qy        732 ProGlyValGlnHisLeuTrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsn 751

Db       2211 TCTGGCCTGAAACATCTCTGGAAGCTCCTTTTTAGCAATCAAAACTTAAAGTACCTCAAT 2270

Qy        752 LeuGlyGlyThrHisLeuLysGluGluAspValArgMetAlaCysGluAlaLeuLysHis 771

Db       2271 CTAGGGAACACTCCCATGAAGGATGATGACATGAAGTTAGCCTGCGAAGCGCTGAAACAT 2330

Qy        772 ProLysCysLeuLeuGluSerLeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyr 791

Db       2331 CCAAAGTGCTCCGTGGAGACTCTGAGGTTGGATTCCTGTGAGTTAACCATCATTGGTTAT 2390

Qy        792 LeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGly 811

Db       2391 GAGATGATCTCCACGCTTCTTATTTCAACCACCAGGCTAAAGTGTCTCAGCCTGGCCAAA 2450

Qy        812 AsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGlnCys 831

Db       2451 AATAGAGTGGGAGTAAAAAGCATGATATCCCTTGGGAATGCCTTGAGTAGCTCAATGTGT 2510

Qy        832 AlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAlaThrGlyCysGlnSerLeu 851

Db       2511 CTACTGCAAAAGTTGATACTGGACAACTGTGGCCTCACACCTGCCAGCTGCCACCTTCTG 2570

Qy        852 AlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeu 871

Db       2571 GTCTCAGCCCTTTTCAGCAACCAGAACTTGACACACCTGTGCCTGTCAAACAACAGCCTG 2630

Qy        872 GlyAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeuGln 891

Db       2631 GGGACTGAAGGAGTGCAACAGCTGTGTCAGTTCCTGAGGAATCCAGAATGTGCTCTCCAG 2690

Qy        892 ArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAla 911

Db       2691 CGGCTGATACTGAATCACTGCAACATTGTAGATGATGCTTATGGCTTCCTGGCAATGAGA 2750

Qy        912 LeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAspAsn 931

Db       2751 CTTGCAAACAACACAAAGCTGACCCACCTGAGCCTGACCATGAACCCCGTAGGGGATGGT 2810

Qy        932 GlyValLysLeuLeuCysGluValMetArgGluProSerCysHisLeuGlnAspLeuGlu 951

Db       2811 GCAATGAAGCTACTGTGTGAAGCTTTAAAGGAACCTACTTGTTACCTTCAAGAACTGGAA 2870

Qy        952 LeuValLysCysHisLeuThrAlaAlaCysCysGluSerLeuSerCysValIleSerArg 971

Db       2871 CTAGTGGACTGCCAACTCACACAGAACTGCTGCGAGGACCTGGCCTGTATGATCACAACA 2930

Qy        972 SerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyValAla 991

Db       2931 ACCAAGCACTTAAAAAGTTTGGATCTTGGTAACAACGCCCTGGGTGACAAAGGAGTCATA 2990

Qy        992 AlaLeuCysGluGlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAla 1011

Db       2991 ACCCTGTGTGAGGGACTGAAGCAAAGTAGCAGCTCCCTGAGGAGACTTGGGTTGGGGGCA 3050
```

```
Qy       1012 CysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArgHis 1031

Db       3051 TGTAAGTTGACTTCCAATTGCTGTGAGGCATTGTCATTGGCCATCTCTTGCAACCCTCAC 3110

Qy       1032 LeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCys 1051

Db       3111 CTGAACAGCCTAAACCTGGTGAAGAATGACTTCAGTACATCGGGGATGTTGAAGCTGTGC 3170

Qy       1052 SerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyr 1071

Db       3171 TCTGCGTTCCAATGCCCTGTCTCTAACCTGGGGATAATTGGCCTGTGGAAGCAGGAGTAC 3230

Qy       1072 ProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuLysProArgValValIle 1091

Db       3231 TATGCCCGAGTGAGAAGACAGCTGGAGGAAGTTGAGTTTGTCAAGCCCCACGTGGTGATT 3290

Qy       1092 AspGlySerTrpHisSerPheAspGluAspAspArgHis 1104

Db       3291 GATGGTGATTGGTATGCTAGTGATGAAGATGACCGAAAC 3329
```

RESULT 12
US-10-399-443-1
; Sequence 1, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-399-443-1

Alignment Scores:

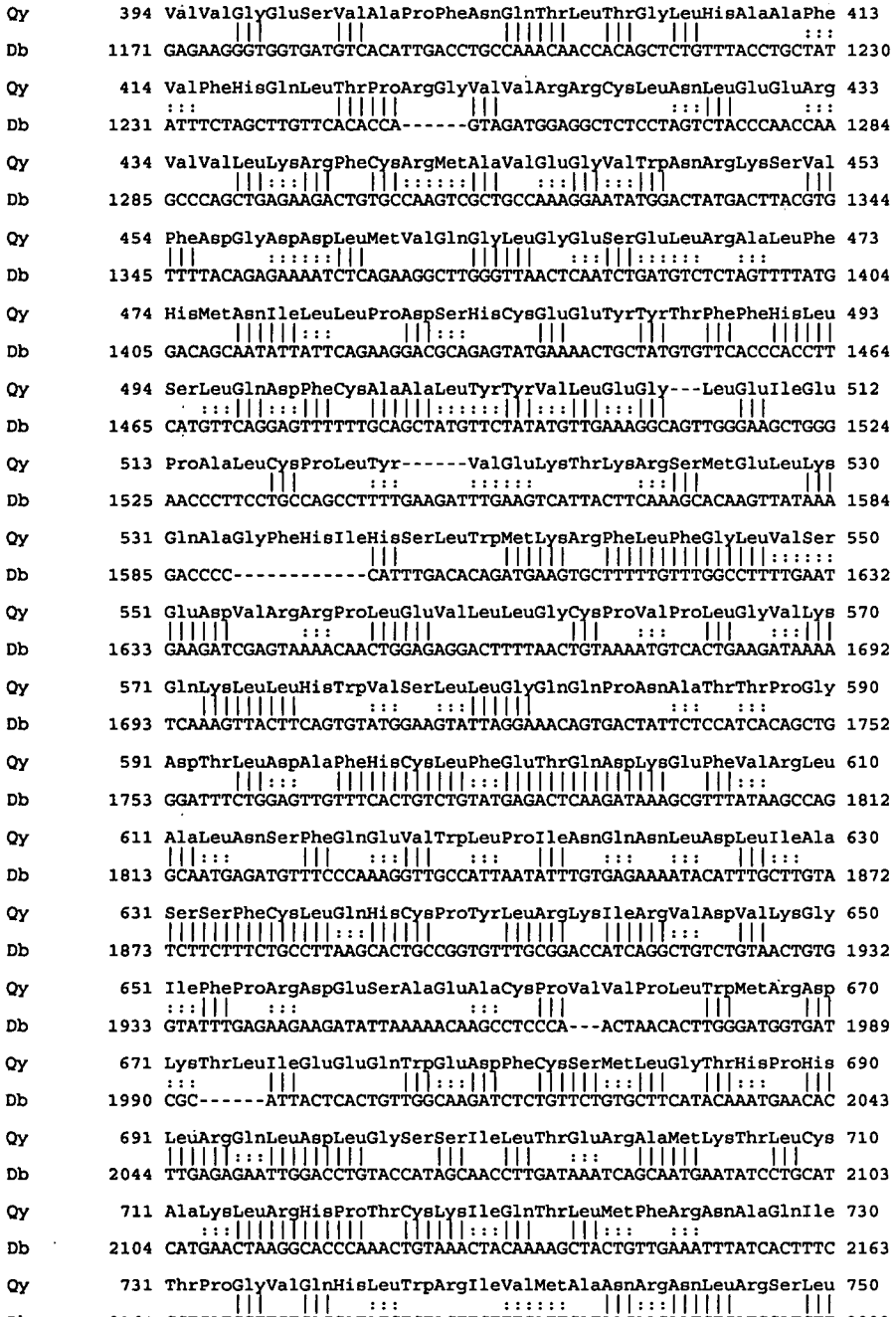
Pred. No.:	1.46e-203	Length:	1157
Score:	2005.00	Matches:	385
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	28.34%	Indels:	0
DB:	17	Gaps:	0

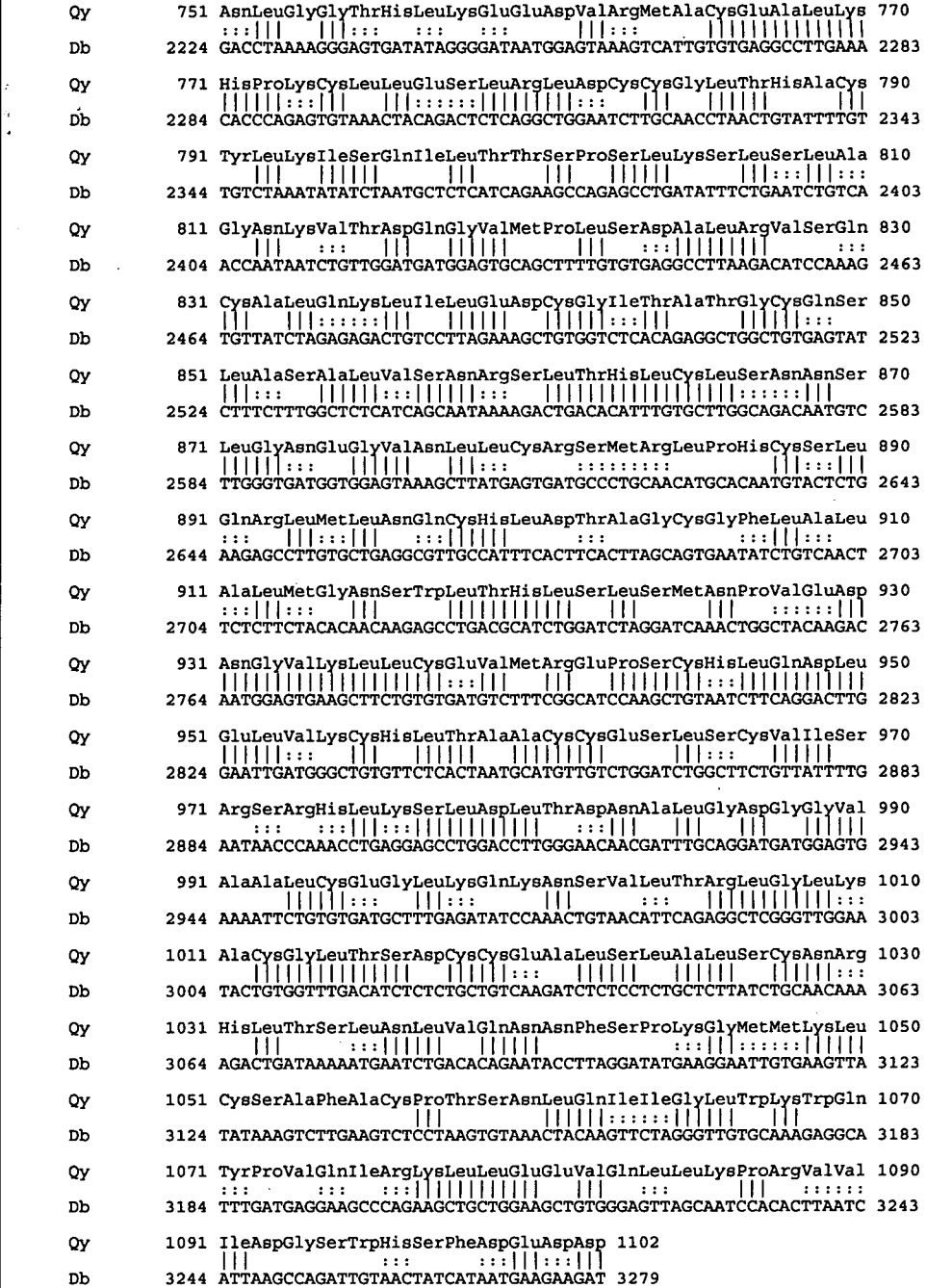
US-10-066-521-6 (1-1344) x US-10-399-443-1 (1-1157)

```
Qy        252 GlnAlaProValThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGly 271

Db          1 CAAGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGT 60

Qy        272 PheAspAspLeuGlySerValLeuAsnAsnAspThrLysLeuCysLysAspTrpAlaGlu 291

Db         61 TTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAG 120

Qy        292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSer 311

Db        121 AAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCC 180

Qy        312 PheLeuIleValThrValArgAspValGlyThrGluLysLeuLysSerGluValValSer 331
```

```
Db        181 TTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCT 240

Qy        332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGlu 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAG 300

Qy        352 ArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGlu 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAG 360

Qy        372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTG 420

Qy        392 GlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAla 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCC 480

Qy        412 AlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGlu 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAG 540

Qy        432 GluArgValValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLys 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAG 600

Qy        452 SerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAla 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCT 660

Qy        472 LeuPheHisMetAsnIleLeuLeuProAspSerHisCysGluGluTyrTyrThrPhePhe 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTC 720

Qy        492 HisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluIle 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATC 780

Qy        512 GluProAlaLeuCysProLeuTyrValGluLysThrLysArgSerMetGluLeuLysGln 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAG 840

Qy        532 AlaGlyPheHisIleHisSerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGlu 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAA 900

Qy        552 AspValArgArgProLeuGluValLeuLeuGlyCysProValProLeuGlyValLysGln 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAG 960

Qy        572 LysLeuLeuHisTrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAsp 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGAC 1020

Qy        592 ThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAla 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCA 1080

Qy        612 LeuAsnSerPheGlnGluValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSer 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCT 1140

Qy        632 SerPheCysLeuGln 636
              ||||||||||||||||
Db       1141 TCCTTCTGCCTCCAG 1155

RESULT 13
US-10-677-943-1
; Sequence 1, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 1157
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-677-943-1

Alignment Scores:
Pred. No.:              1.46e-203       Length:         1157
Score:                  2005.00         Matches:        385
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            28.34%          Indels:         0
DB:                     17              Gaps:           0

US-10-066-521-6 (1-1344) x US-10-677-943-1 (1-1157)

Qy        252 GlnAlaProValThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGly 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAAGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGT 60

Qy        272 PheAspAspLeuGlySerValLeuAsnAsnAspThrLysLeuCysLysAspTrpAlaGlu 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAG 120

Qy        292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSer 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCC 180

Qy        312 PheLeuIleValThrValArgAspValGlyThrGluLysLeuLysSerGluValValSer 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCT 240

Qy        332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGlu 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAG 300

Qy        352 ArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGlu 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAG 360

Qy        372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTG 420

Qy        392 GlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAla 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCC 480

Qy        412 AlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGlu 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAG 540

Qy        432 GluArgValValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLys 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAG 600

Qy        452 SerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAla 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

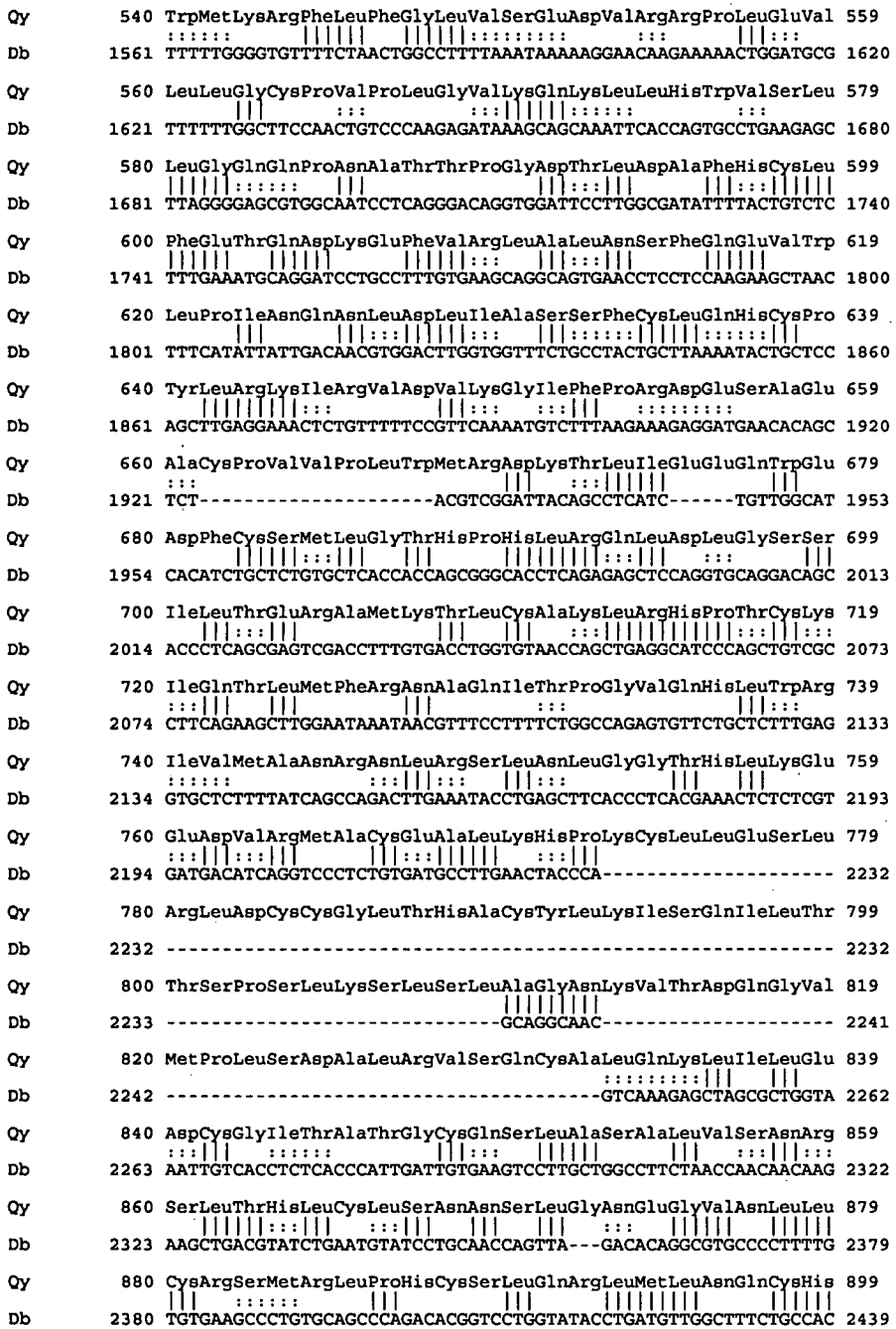
```
Db        601 TCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCT 660

Qy        472 LeuPheHisMetAsnIleLeuLeuProAspSerHisCysGluGluTyrTyrThrPhePhe 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTC 720

Qy        492 HisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluIle 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATC 780

Qy        512 GluProAlaLeuCysProLeuTyrValGluLysThrLysArgSerMetGluLeuLysGln 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAG 840

Qy        532 AlaGlyPheHisIleHisSerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGlu 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAA 900

Qy        552 AspValArgArgProLeuGluValLeuLeuGlyCysProValProLeuGlyValLysGln 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAG 960

Qy        572 LysLeuLeuHisTrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAsp 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGAC 1020

Qy        592 ThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAla 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCA 1080

Qy        612 LeuAsnSerPheGlnGluValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSer 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCT 1140

Qy        632 SerPheCysLeuGln 636
              |||||||||||||||
Db       1141 TCCTTCTGCCTCCAG 1155

RESULT 14
US-10-794-342-2
; Sequence 2, Application US/10794342
; Publication No. US20040253615A1
; GENERAL INFORMATION:
;  APPLICANT: Inohara, Naohiro
;  APPLICANT:  Nunez, Gabriel
;  TITLE OF INVENTION: NOD Nucleic Acids and Polypeptides
;  FILE REFERENCE: UM-08922
;  CURRENT APPLICATION NUMBER: US/10/794,342
;  CURRENT FILING DATE:  2004-03-05
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 3521
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-794-342-2

Alignment Scores:
Pred. No.:              5.45e-190       Length:         3521
Score:                  1885.50         Matches:        422
Percent Similarity:     56.65%          Conservative:   208
Best Local Similarity:  37.95%          Mismatches:     443
Query Match:            26.65%          Indels:         39
DB:                     18              Gaps:           13

US-10-066-521-6 (1-1344) x US-10-794-342-2 (1-3521)

Qy          2 GluGlyAspLysSerLeuThrPheSerSerTyrGlyLeuGlnTrpCysLeuTyrGluLeu 21
              :::       |||      |||      :::|||||         |||   ||||||
Db         28 GATTCATCATCATCTTCTTTCTTTCCTGATTTTGGGCTGCTATTGTATTTGGAGGAGCTA 87

Qy         22 AspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysLysSerSerGluSerThr 41
              :::|||||||||      |||||||||   |||      |||::::::   |||

Db         88 AACAAAGAGGAATTAAATACATTCAAG---TTATTCCTAAAGGAGACCATGGAACCTGAG 144

Qy         42 ThrCysSerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeuLeu 61
                          |||      |||::::::   |||      |||   ||||||   |||
Db        145 CATGGCCTGACACCCTGGAATGAAGTGAAGAAGGCCAGGCGGGAGGACCTGGCCAATTTG 204

Qy         62 LeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGluAsn 81
              :::   :::||||||         ||||||:::   |||:::   ||||||
Db        205 ATGAAGAAATATTATCCAGGAGAGAAAGCCTGGAGTGTGTCTCTCAAAATCTTTGGCAAG 264

Qy         82 MetAsnLeuArgThrLeuSerGluLysAlaArgAspAspMetLysLysIleSerGlnAla 101
              |||||||||:::   |||   |||:::|||:::::::::::::         :::|||
Db        265 ATGAACCTGAAGGATCTGTGTGAGAGAGCGAAAGAAGAGATCAACTGGTCGGCCCAGACT 324

Qy        102 MetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGluIleSerGlnAlaMet 121
              :::      :::    |||    |||   ||||||:::|||
Db        325 ATAGGACCAGATGATGCCAAGGCTGGAGAGACACAAGAA---------------------- 363

Qy        122 GluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGlyHisGlyGlyAspThrTrp 141
              :::||||||                                    ||||||
Db        364 GATCAGGAGGCAGTGCTG----------------------------GGTGATGGAACA 393

Qy        142 AspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspValArgArgSerPhe 161
              :::|||:::::   :::      ||||||              |||   :::::::|||
Db        394 GAATACAGAAATAGAATAAAGGAAAAATTTTGCATCACTTGGGAC---AAGAAGTCTTTG 450

Qy        162 GluAsnThrAlaAlaAspTrp-----------------ProGluMetGlnThrLeuAla 175
                          |||:::                  :::   :::   |||
Db        451 GCTGGAAAGCCTGAAGATTTCCATCATGGAATTGCAGAGAAAGATAGAAAACTGTTGGAA 510

Qy        176 GlyAlaPheAspSerAsp---ArgTrpGlyPheArgProArgThrValValLeuHisGly 194
              |||||  |||   :::   |||   :::|||:::    |||||||||   |||
Db        511 CACTTGTTCGATGTGGATGTCAAAACCGGTGCACAGCCACAGATCGTGGTGCTTCAGGGA 570

Qy        195 LysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGly 214
                 :::|||:::||||||:::   |||   |||:::   :::|||   |||||||:::|||
Db        571 GCTGCTGGAGTTGGGAAAACAACCTTGGTGAGAAAGGCAATGTTAGATTGGGCAGAGGGC 630

Qy        215 GlyLeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMetGlnArg 234
              |||||||||       |||   |||||||||:::|||       ||||||:::   :::
Db        631 AGTCTCTACCAGCAGAGGTTTAAGTATGTTTTTTATCTCAATGGGAGAGAAATTAACCAG 690

Qy        235 LysLysGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGlnAlaPro 254
              ||||||  |||      :::   ||||||:::::||||||   ::::::   |||
Db        691 CTGAAAGAGAGAAGCTTTGCTCAATTGATATCAAAGGACTGGCCCAGCACAGAAGGCCCC 750

Qy        255 ValThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAsp 274
              :::   |||||||||   :::|||       |||||||||||||||||   ||||||:::
Db        751 ATTGAAGAAATCATGTACCAGCCAAGTAGCCTCTTGTTTATTATTGACAGTTTCGATGAA 810

Qy        275 LeuGlySerValLeuAsnAsn---AspThrLysLeuCysLysAspTrpAlaGluLysGln 293
              |||                  :::      ||||||:::||||||   ::::::
Db        811 CTGAACTTTGCCTTTGAAGAACCTGAGTTTGCACTGTGCGAAGACTGGACCCAAGAACAC 870

Qy        294 ProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeu 313
              |||       |||:::   |||||||||||||||||:::|||||||||:::   |||
Db        871 CCAGTGTCCTTCCTCATGAGTAGTTTGCTGAGGAAAGTGATGCTCCCTGAGGCATCCTTA 930

Qy        314 IleValThrValArgAspValGlyThrGluLysLeuLysSerGluValValSerProArg 333
              :::||||||   |||         :::::::::||||||      :::   :::
Db        931 TTGGTGACAACAAGACTCACAACTTCTAAGAGACTAAAGCAGTTGTTGAAGAATCACCAT 990

Qy        334 TyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGluArgGly 353
              |||:::   :::   |||:::|||   :::   |||         :::   :::
Db        991 TATGTAGAGCTACTAGGAATGTCTGAGGATGCAAGAGAGGAGTATATTTACCAGTTTTTT 1050

Qy        354 IleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeu 373
                    :::       :::      ::::::   :::|||      |||
Db       1051 GAAGATAAGAGGTGGGCCATGAAAGTATTCAGTTCACTAAAAAGCAATGAGATGCTGTTT 1110

Qy        374 AspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAsp 393
                 ||||||||||||   |||         |||      |||:::   |||
Db       1111 AGCATGTGCCAAGTCCCCCTAGTGTGCTGGGCCGCTTGTACTTGTCTGAAGCAGCAAATG 1170
```


Qy 394 ValValGlyGluSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPhe 413
Db 1171 GAGAAGGGTGGTGATGTCACATTGACCTGCCAAACAACCACAGCTCTGTTTACCTGCTAT 1230
Qy 414 ValPheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGluGluArg 433
Db 1231 ATTTCTAGCTTGTTCACACCA------GTAGATGGAGGCTCTCCTAGTCTACCCAACCAA 1284
Qy 434 ValValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerVal 453
Db 1285 GCCCAGCTGAGAAGACTGTGCCAAGTCGCTGCCAAAGGAATATGGACTATGACTTACGTG 1344
Qy 454 PheAspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPhe 473
Db 1345 TTTTACAGAGAAAATCTCAGAAGGCTTGGGTTAACTCAATCTGATGTCTCTAGTTTTATG 1404
Qy 474 HisMetAsnIleLeuLeuProAspSerHisCysGluGluTyrTyrThrPheHisLeu 493
Db 1405 GACAGCAATATTATTCAGAAGGACGCAGAGTATGAAAACTGCTATGTGTTCACCCACCTT 1464
Qy 494 SerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGluGly---LeuGluIleGlu 512
Db 1465 CATGTTCAGGAGTTTTTTGCAGCTATGTTCTATATGTTGAAAGGCAGTTGGGAAGCTGGG 1524
Qy 513 ProAlaLeuCysProLeuTyr------ValGluLysThrLysArgSerMetGluLeuLys 530
Db 1525 AACCCTTCCTGCCAGCCTTTTGAAGATTTGAAGTCATTACTTCAAAGCACAAGTTATAAA 1584
Qy 531 GlnAlaGlyPheHisIleHisSerLeuTrpMetLysArgPheLeuPheGlyLeuValSer 550
Db 1585 GACCCC-----------CATTTGACACAGATGAAGTGCTTTTTGTTTGGCCTTTTGAAT 1632
Qy 551 GluAspValArgArgProLeuGluValLeuLeuGlyCysProValProLeuGlyValLys 570
Db 1633 GAAGATCGAGTAAAACAACTGGAGAGGACTTTTAACTGTAAAATGTCACTGAAGATAAAA 1692
Qy 571 GlnLysLeuLeuHisTrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGly 590
Db 1693 TCAAAGTTACTTCAGTGTATGGAAGTATTAGGAAACAGTGACTATTCTCCATCACAGCTG 1752
Qy 591 AspThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeu 610
Db 1753 GGATTTCTGGAGTTGTTTCACTGTCTGTATGAGACTCAAGATAAAGCGTTTATAAGCCAG 1812
Qy 611 AlaLeuAsnSerPheGlnGluValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAla 630
Db 1813 GCAATGAGATGTTTCCCAAAGGTTGCCATTAATATTTGTGAGAAAATACATTTGCTTGTA 1872
Qy 631 SerSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArgValAspValLysGly 650
Db 1873 TCTTCTTTCTGCCTTAAGCACTGCCGGTGTTTGCGGACCATCAGGCTGTCTGTAACTGTG 1932
Qy 651 IlePheProArgAspGluSerAlaGluAlaCysProValValProLeuTrpMetArgAsp 670
Db 1933 GTATTTGAGAAGAAGATATTAAAAACAAGCCTCCCA---ACTAACACTTGGGATGGTGAT 1989
Qy 671 LysThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGlyThrHisProHis 690
Db 1990 CGC------ATTACTCACTGTTGGCAAGATCTCTGTTCTGTGCTTCATACAAATGAACAC 2043
Qy 691 LeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLysThrLeuCys 710
Db 2044 TTGAGAGAATTGGACCTGTACCATAGCAACCTTGATAAATCAGCAATGAATATCCTGCAT 2103
Qy 711 AlaLysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIle 730
Db 2104 CATGAACTAAGGCACCCAAACTGTAAACTACAAAAGCTACTGTTGAAATTTATCACTTTC 2163
Qy 731 ThrProGlyValGlnHisLeuTrpArgIleValMetAlaAsnArgAsnLeuArgSerLeu 750
Db 2164 CCTGATGGTTGTCAGGATATCTCTACTTCTTTGATTCATAACAAGAATCTGATGCATCTT 2223


Qy 751 AsnLeuGlyGlyThrHisLeuLysGluGluAspValArgMetAlaCysGluAlaLeuLys 770
Db 2224 GACCTAAAAGGGAGTGATATAGGGGATAATGGAGTAAAGTCATTGTGTGAGGCCTTGAAA 2283
Qy 771 HisProLysCysLeuLeuGluSerLeuArgLeuAspCysCysGlyLeuThrHisAlaCys 790
Db 2284 CACCCAGAGTGTAAACTACAGACTCTCAGGCTGGAATCTTGCAACCTAACTGTATTTTGT 2343
Qy 791 TyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeuAla 810
Db 2344 TGTCTAAATATATCTAATGCTCTCATCAGAAGCCAGAGCCTGATATTTCTGAATCTGTCA 2403
Qy 811 GlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGln 830
Db 2404 ACCAATAATCTGTTGGATGATGGAGTGCAGCTTTGTGTGAGGCCTTAAGACATCCAAAG 2463
Qy 831 CysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAlaThrGlyCysGlnSer 850
Db 2464 TGTTATCTAGAGAGACTGTCCTTAGAAAGCTGTGGTCTCACAGAGGCTGGCTGTGAGTAT 2523
Qy 851 LeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSer 870
Db 2524 CTTTCTTTGGCTCTCATCAGCAATAAAAGACTGACACATTTGTGCTTGGCAGACAATGTC 2583
Qy 871 LeuGlyAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeu 890
Db 2584 TTGGGTGATGGTGGAGTAAAGCTTATGAGTGATGCCCTGCAACATGCACAATGTACTCTG 2643
Qy 891 GlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLeu 910
Db 2644 AAGAGCCTTGTGCTGAGGCGTTGCCATTTCACTTCACTTAGCAGTGAATATCTGTCAACT 2703
Qy 911 AlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAsp 930
Db 2704 TCTCTTCTACACAACAAGAGCCTGACGCATCTGGATCTAGGATCAAACTGGCTACAAGAC 2763
Qy 931 AsnGlyValLysLeuLeuCysGluValMetArgGluProSerCysHisLeuGlnAspLeu 950
Db 2764 AATGGAGTGAAGCTTCTGTGTGATGTCTTTCGGCATCCAAGCTGTAATCTTCAGGACTTG 2823
Qy 951 GluLeuValLysCysHisLeuThrAlaAlaCysCysGluSerLeuSerCysValIleSer 970
Db 2824 GAATTGATGGGCTGTGTTCTCACTAATGCATGTTGTCTGGATCTGGCTTCTGTTATTTTG 2883
Qy 971 ArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyVal 990
Db 2884 AATAACCCAAACCTGAGGAGCCTGGACCTTGGGAACAACGATTTGCAGGATGATGGAGTG 2943
Qy 991 AlaAlaLeuCysGluGlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLys 1010
Db 2944 AAAATTCTGTGTGATGCTTTGAGATATCCAAACTGTAACATTCAGAGGCTCGGGTTGGAA 3003
Qy 1011 AlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArg 1030
Db 3004 TACTGTGGTTTGACATCTCTCTGCTGTCAAGATCTCTCCTCTGCTCTTATCTGCAACAAA 3063
Qy 1031 HisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLeu 1050
Db 3064 AGACTGATAAAAATGAATCTGACACAGAATACCTTAGGATATGAAGGAATTGTGAAGTTA 3123
Qy 1051 CysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGln 1070
Db 3124 TATAAAGTCTTGAAGTCTCCTAAGTGTAAACTACAAGTTCTAGGGTTGTGCAAAGAGGCA 3183
Qy 1071 TyrProValGlnIleArgLysLeuGluGluValGlnLeuLeuLysProArgValVal 1090
Db 3184 TTTGATGAGGAAGCCCAGAAGCTGCTGGAAGCTGTGGGAGTTAGCAATCCACACTTAATC 3243
Qy 1091 IleAspGlySerTrpHisSerPheAspGluAspAsp 1102
Db 3244 ATTAAGCCAGATTGTAACTATCATAATGAAGAAGAT 3279

RESULT 15

```
US-10-124-498-23
; Sequence 23, Application US/10124498
; Publication No. US20030017983A1
; GENERAL INFORMATION:
;  APPLICANT: Bertin, John
;  APPLICANT:  Wang, Weiye
;  APPLICANT:  Blatcher, Maria
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
;  TITLE OF INVENTION:  PROTEIN FAMILY AND USES THEREOF
;  FILE REFERENCE: 07334-367001
;  CURRENT APPLICATION NUMBER: US/10/124,498
;  CURRENT FILING DATE:  2002-04-17
;  PRIOR APPLICATION NUMBER: 10/066,521
;  PRIOR FILING DATE: 2002-01-31
;  PRIOR APPLICATION NUMBER: 60/318,645
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: 60/265,231
;  PRIOR FILING DATE: 2001-01-31
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 3368
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (70)...(3051)
US-10-124-498-23

Alignment Scores:
Pred. No.:              7.21e-142      Length:          3368
Score:                  1435.00        Matches:         349
Percent Similarity:     48.05%         Conservative:    204
Best Local Similarity:  30.32%         Mismatches:      448
Query Match:            20.29%         Indels:          150
DB:                     14             Gaps:            15

US-10-066-521-6 (1-1344) x US-10-124-498-23 (1-3368)

Qy          9 PheSerSerTyrGlyLeuGlnTrpCysLeuTyrGluLeuAspLysGluGluPheGlnThr 28
              ||||||   :::|||||||   |||  |||  ||||||  ||||||||||||:::
Db         85 TTCTCTGATTTTGGTCTTATGTGGTATCTGGAGGAGCTCAAAAAGGAGGAGTTCAGGAAA 144

Qy         29 PheLysGluLeuLeuLysLysLysSerSerGluSerThrThrCysSerIleProGlnPhe 48
              |||||||||   ||||||:::   :::   :::           ||||||
Db        145 TTTAAAGAACATCTCAAGCAAATGACTTTGCAGCTTGAACTCAAGCAGATTCCCTGGACT 204

Qy         49 GluIleGluAsnAlaAsnValGluCysLeuAlaLeuLeuLeuHisGluTyrTyrGlyAla 68
              |||::::::   |||:::   |||   ||||||   ||||||   ::::::|||
Db        205 GAGGTCAAAAAAGCATCCCGGGAAGAACTTGCAAACCTCTTGATCAAGCACTATGAAGAA 264

Qy         69 SerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArgThrLeuSer 88
                 ||||||    ::::::   ||||||:::   |||
Db        265 CAACAAGCTTGGAACATAACCTTAAGAATCTTTCAAAAGATG------------------ 306

Qy         89 GluLysAlaArgAspAspMetLysLysIleSerGlnAlaMetGluGlnGluGlyAlaThr 108
                          |||   |||   :::         :::   :::|||
Db        307 --------------GATAGAAAGGATCTCTGCATGAAGGTCATGAGGGAGAGAACAGGA 351

Qy        109 AlaAlaGluThrGluGluGlnGluIleSerGlnAlaMetGluGlnGluGlyAlaThrAla 128
                    :::|||   :::             |||         :::
Db        352 TACACAAAGACCTATCAAGCTCACGCAAAGCAGAAATTCAGCCGC--------------- 396

Qy        129 AlaGluThrGluGluGlnGlyHisGlyGlyAspThrTrpAspTyrLysSerHisValMet 148
                                                  |||     ||||||
Db        397 --------------------------------TTATGGTCCAGCAAGTCTGTCACTGAG 423

Qy        149 ThrLysPheAlaGluGluGluAspValArgArgSerPheGluAsnThrAlaAlaAspTrp 168
                          ||||||:::|||::::::
Db        424 ATTCACCTATACTTTGAGGAGGAAGTCAAGCAAGAA---------------------- 459

Qy        169 ProGluMetGlnThrLeuAlaGlyAlaPheAspSerAspArgTrpGlyPheArgProArg 188
                 |||         |||         |||               |||   :::||||||

Db        460 ---GAATGTGACCATTTGGACCGCCTTTTTGCTCCCAAGGAAACTGGGAAACAGCCACGT 516

Qy        189 ThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleVal 208
              ||||||::::::   |||       ||||||||||:::   |||       :::::::::
Db        517 ACAGTGATTATTCAAGGACCACAAGGAATTGGAAAAACGACACTCCTGATGAAGCTGATG 576

Qy        209 LeuCysTrpAlaGlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePheLeuPro 228
              :::   |||:::         :::::::::       |||   |||   |||:::
Db        577 ATGGCCTGGTCGGACAACAAGATCTTTCGGGATAGGTTCCTGTACACGTTCTATTTCTGC 636

Qy        229 ValArgGluMetGlnArgLysLysGluSerSerValThrGluPheIleSerArgGluTrp 248
                 ||||||::::::           :::|||:::   :::   ||||||||||||||
Db        637 TGCAGAGAACTGAGGGAGTTGCCGCCAACGAGTTTGGCTGACTTGATTTCCAGAGAGTGG 696

Qy        249 ProAspSerGlnAlaProValThrGluIleMetSerArgProGluArgLeuLeuPheIle 268
              ||||||       ||||||:::||||||||::|||:::|||||||||||||||||:::
Db        697 CCTGACCCCGCTGCTCCTATAACAGAGATCGTGTCTCAACCGGAGAGACTCTTGTTCGTC 756

Qy        269 IleAspGlyPheAspAspLeuGlySerValLeuAsnAsn---AspThrLysLeuCysLys 287
              ||||||   |||::::::|||         ||||||      |||:::   ||||||
Db        757 ATCGACAGCTTCGAAGAGCTGCAGGGCGGCTTGAACGAACCCGATTCGGATCTGTGTGGT 816

Qy        288 AspTrpAlaGluLysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeu 307
              |||       ||||||:::|||         |||:::   ||||||||||||||   :::
Db        817 GACTTGATGGAGAAACGGCCGGTGCAGGTGCTTCTGAGCAGTTTGCTGAGGAAGAAGATG 876

Qy        308 LeuProGluSerPheLeuIleValThrValArgAspValGlyThrGluLysLeuLysSer 327
              |||||||||:::   |||::::::   ::::::   |||       ::::::|||:::
Db        877 CTCCCGGAGGCCTCCCTGCTCATCGCCATCAAACCCGTGTGCCCGAAGGAGCTCCGGGAT 936

Qy        328 GluValValSerProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHis 347
              :::|||                         |||||   :::         |||:::
Db        937 CAGGTGACGATCTCAGAAATCTACCAGCCCCGGGGATTCAACGAGAGTGATAGGTTAGTG 996

Qy        348 LeuLeuLeuGluArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMet 367
                                        :::     :::         :::
Db        997 TATTTCTGCTGTTTCTTCAAAGACCCGAAAAGAGCCATGGAAGCCTTCAATCTTGTAAGA 1056

Qy        368 AsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysVal 387
                 :::   :::|||         ||||||:::|||   :::       :::::|||
Db       1057 GAAAGTGAACAGCTGTTTTCCATATGCCAAATCCCGCTCCTCTGCTGGATCCTGTGTACC 1116

Qy        388 AlaLeuGlnLeuGlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeuThr 407
              :::|||:::   :::         |||:::   :::|||         |||:::   |||
Db       1117 AGTCTGAAGCAAGAGATGCAGAAAGGAAAAGACCTGGCCCTGACCTGCCAGAGCACTACC 1176

Qy        408 GlyLeuHisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCys 427
                 ::::::::::::|||||||||:::     ||||||   |||
Db       1177 TCTGTGTACTCCTCTTTCGTCTTTAACCTGTTCACACCTGAGGGTGCCGAGGGCCCGACT 1236

Qy        428 LeuAsnLeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGlyVal 447
                       :::   :::     ||||||     |||   :::|||   |||||:::
Db       1237 CCGCAAACCCAGCACCAG------CTGAAGGCCCTGTGCTCCCTGGCTGCAGAGGGTATG 1290

Qy        448 TrpAsnArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGluSer 467
              |||         |||     |||||||||       |||:::   ::::::
Db       1291 TGGACAGACACATTTGAGTTTTGTGAAGACGACCTCCGGAGAAATGGGGTTGTTGACGCT 1350

Qy        468 GluLeuArgAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCysGluGluTyr 487
              ::::::   ||||||           |||||||||                  |||
Db       1351 GACATCCCTGCGCTGCTGGGCACCAAGATACTTCTGAAGTACGGGGAGCGTGAGAGCTCC 1410

Qy        488 TyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGlu 507
              |||   |||   |||:::   :::|||:::|||||||||||||:::|||:::|||:::
Db       1411 TACGTGTTCCTCCACGTGTGTATCCAGGAGTTCTGTGCCGCCTTGTTCTATTTGCTCAAG 1470

Qy        508 GlyLeuGluIleGluPro----------------------AlaLeuCysProLeuTyr 519
                          |||                         |||
Db       1471 AGCCACCTTGATCATCCTCACCCAGCTGTGAGATGTGTACAGGAATTGCTAGTTGCCAAT 1530

Qy        520 ValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeu 539
              ||||||   :::|||:::                                 |||   :::
Db       1531 TTTGAAAAAGCAAGGAGAGCA----------------------------CATTGGATT 1560
```



Search completed: February 4, 2005, 21:43:52
Job time : 1762 secs